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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 15, 2003, 18:20:48 ; Search time 1282 Seconds
(without alignments)
9874.977 Million cell updates/sec

Title: US-09-884-987-1_COPY_765_1199
Perfect score: 435
Sequence: 1 aagagaaggaagtagacagaa.....atgaaatccaaagcttggtc 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl : *
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sv.*
13: gb.un.*
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15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
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22: em.ov.*
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27: em.sts.*
28: em.un.*
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31: em.htg_in.*
32: em.htg_in.*
33: em.htg_mus.*
34: em.htg_pln.*
35: em.htg_rod.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	435	100.0	698	9	HSFASCD3	247995 H.sapiens F
2	435	100.0	761	9	HSFASCD3	247994 H.sapiens F
3	435	100.0	836	9	HSFAS46DL	270520 H.sapiens F
4	435	100.0	857	9	HSFAS346	X83491 H.sapiens m
5	435	100.0	899	9	HSFAS4DEL	270519 H.sapiens F
6	435	100.0	920	9	HSFAS34	X83490 H.sapiens m
7	435	100.0	945	9	HSFASCD31	247993 H.sapiens F
8	435	100.0	1008	6	E05336	E05336 DNA encodin
9	435	100.0	1104	9	HSFAS6	X83493 H.sapiens m
10	435	100.0	1457	6	E35160	E35160 Method for
11	435	100.0	2471	6	I58632	I58632 Sequence 18
12	435	100.0	2471	6	I63530	I63530 Sequence 18
13	435	100.0	2534	6	A87646	A87646 Sequence 4
14	435	100.0	2534	6	ARI163572	ARI163572 Sequence
15	435	100.0	2534	6	ARI173438	ARI173438 Sequence
16	435	100.0	2534	6	E05110	E05110 cDNA encodi
17	435	100.0	2534	6	E09121	E09121 cDNA encodi
18	435	100.0	2534	9	HUMFASANT	M67454 Human Fas a
19	435	100.0	2551	6	ARI143111	ARI143111 Sequence
20	435	100.0	2551	9	HSAP01	X63717 H.sapiens m
21	435	100.0	2719	9	BC012479	BC012479 Homo sapi
22	435	100.0	8282	6	AX146813	AX146813 Sequence
23	435	100.0	8345	6	AX146814	AX146814 Sequence
24	433.4	99.6	1468	6	AX060536	AX060536 Sequence
25	433.4	99.6	1483	6	AX060538	AX060538 Sequence
26	433.4	99.6	3009	6	AX060540	AX060540 Sequence
27	433.4	99.6	3009	6	AX060542	AX060542 Sequence
28	375	86.2	983	9	HSFASAP0A	Z66556 H.sapiens F
29	369.4	84.9	996	9	AB031420	AB031420 Macaca fa
30	366.2	84.2	1342	9	AF344850	AF344850 Macaca ne
31	364.6	83.8	1068	9	AF326208	AF326208 Macaca as
32	363.6	83.6	1005	9	AF332357	AF332357 Macaca ar
33	361.4	83.1	1077	9	AF007572	AF007572 Macaca mu
34	361.4	83.1	1367	9	AF344833	AF344833 Macaca mu
35	359.8	82.7	1361	9	AF344843	AF344843 Cercocebu
36	354	81.4	975	6	AX331556	AX331556 Sequence
37	354	81.4	975	6	AX336715	AX336715 Sequence
38	354	81.4	975	9	HSFAS47	X83492 H.sapiens m
39	334.8	77.0	1840	9	HSAPT9	X81342 H.sapiens A
40	334.8	77.0	1846	11	G75384	G75384 csntnfrsf6
41	334.8	77.0	2774	9	HSFASX9	X82286 H.sapiens F
42	334.8	77.0	187313	9	AL157394	AL157394 Human DNA
43	307.8	70.8	1324	9	AF344835	AF344835 Aotus tri
44	285	65.5	960	4	AB021298	AB021298 Oryctolag
45	285	65.5	963	4	AB021299	AB021299 Oryctolag

ALIGNMENTS

RESULT 1
LOCUS HSFASCD3
DEFINITION H.sapiens FAS Del3 mRNA.
ACCESSION 247995
VERSION 247995.1 GI:728580
KEYWORDS FAS gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS Ruberti,G.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,


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/standard_name="FAS/Apo 1"
/number=1
/evidence-experimental
31..196
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/number=2
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197..258
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/number=5
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259..321
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322..404
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Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 324 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAAGCAAGGTTCTCAT 383
QY 61 GAATCTCCAACTTAAATCCTGGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120
DB 384 GAATCTCCAACTTAAATCCTGGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 443
QY 121 AAATATATCAGACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180
DB 444 AAATATATCAGACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 503
QY 181 AAGATGTGTCAATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 504 AAGATGTGTCAATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 563
QY 241 GCAGAACAGAAAGTTCAACTGCTGTAATGGCATCAACTTTCATGGAAGAAAGAAAGCG 300
DB 564 GCAGAACAGAAAGTTCAACTGCTGTAATGGCATCAACTTTCATGGAAGAAAGAAAGCG 623
QY 301 TATGACATGATTAAGATCTCAAAAAGCCATCTTTGTACTCTTGCAGAGAAATTT 360
DB 624 TATGACATGATTAAGATCTCAAAAAGCCATCTTTGTACTCTTGCAGAGAAATTT 683
QY 361 CAGACTATCATCTCAAGACATTAAGTACTGACTCAGAAAAATTCAGAAATTCAGAAATGAA 420
DB 684 CAGACTATCATCTCAAGACATTAAGTACTGACTCAGAAAAATTCAGAAATTCAGAAATGAA 743
QY 421 ATCCAAAGCTTGCTC 435
DB 744 ATCCAAAGCTTGCTC 758
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RESULT 3
HSFAS46DL
LOCUS
DEFINITION H.sapiens FAS/Apo 1 mRNA for FAS soluble protein (clone FAS
Exo4,6Del).
ACCESSION 270520
VERSION 1
KEYWORDS FAS soluble protein; FAS/Apo 1 gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 836)
AUTHORS Papoff,G., Cascino,I., Eramo,A., Starace,G., Lynch,D.H. and
Ruberti,G.
TITLE A N-terminal domain shared by Fas soluble variants prevents cell
death in vivo
J. Immunol. (1996) In press
REFERENCE 2 (bases 1 to 846)
AUTHORS Ruberti,G.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R.,
Immunology, viale C.Marx 43, Rome, Italy, I-00137
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/isolate="LN"
/db_xref="taxon:9606"
/chromosome="10"
/clone="FAS Exo4,6Del"
/cell_type="PHA-activated PBMC"
1..399
/note="Alternative splicing variant of FAS gene missing
exons 4 and 6. Exon 5 translated in a different frame up
to a new stop codon at the beginning of exon 7."
/codon_start=1
/evidence-experimental
/product="FAS soluble protein"
/protein_id="CAA94431.1"
/db_xref="GI:1418816"
/db_xref="SPTREMBL:Q16652"
/translation="MLGIWTLPLVLTSLVRLSKSVNAQVTDINSGLELRKKTVTTV.
ETONLEGLHHDGQFCHKPCPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKCR
RCRLCDEGHVNMESSRNAHSPATPSARKK"
<1..30
/number=1
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31..196
/number=2
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197..334
/number=3
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335..396
/note="Translated in a different frame in this variant."
/number=5
/evidence-experimental
397..479
/note="Not translated in this variant as there is a stop
codon at 397."
/number=7
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480..504
/note="Not translated in this variant."
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/note="Not translated in this variant."
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BASE COUNT
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.7e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCAT 60
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Db 399 AAGAGAAAGGAGTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCAT 458
   |||||

QY 61 GAATCTCCAACCTTAATCTGGAACAGTGCATCAATATTTATCTGATGTTGACTTGAGT 120
   |||||
Db 459 GAATCTCCAACCTTAATCTGGAACAGTGCATCAATATTTATCTGATGTTGACTTGAGT 518
   |||||

QY 121 AAATATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 180
   |||||
Db 519 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 578
   |||||

QY 181 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 240
   |||||
Db 579 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 638
   |||||

QY 241 GCAGAACAGAAAGTTCAACTGCTCTGTAATGGCATCAACTTCATGGAAGAAAGAGCG 300
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Db 639 GCAGAACAGAAAGTTCAACTGCTCTGTAATGGCATCAACTTCATGGAAGAAAGAGCG 698
   |||||

QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAAATT 360
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Db 699 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAAATT 758
   |||||

QY 361 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 420
   |||||
Db 759 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 818
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QY 421 ATCCAAAGCTTGGTC 435
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Db 819 ATCCAAAGCTTGGTC 833
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RESULT 4
HSFAS346      857 bp mRNA linear PRI 28-NOV-1995
LOCUS
DEFINITION H.sapiens mRNA for Fas/Apo-1 (clone pCRTM11-Fasdelta(3,4,6)).
ACCESSION X83491
VERSION X83491.1 GI:971455
KEYWORDS FAS gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Cheng, J., Zhou, T., Liu, C., Shapiro, J.P., Brauer, M.J., Kiefer, M.C.,
Barr, P.J. and Mountz, J.D.
TITLE Protection from Fas-mediated apoptosis by a soluble form of the Fas
molecule
JOURNAL Science 263 (5154), 1759-1762 (1999)
MEDLINE 94182136
PUBMED 7510905
REFERENCE 2 (bases 1 to 857)
AUTHORS Cheng, J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) J. Cheng, University of Alabama at
Birmingham, Division of Clinical Immunol. & Rheum., UAB Station,
LHRB 473, Birmingham AL 35294-0007, USA
3 (bases 1 to 857)
AUTHORS Liu, C., Cheng, J. and Mountz, J.D.
TITLE Differential expression of human Fas mRNA species upon peripheral
Blood mononuclear cell activation
JOURNAL Biochem. J. 310 (Pt 3), 957-963 (1995)
MEDLINE 96013198
PUBMED 7575433
COMMENT Related sequences: M67454 and X63717.
FEATURES Location/Qualifiers
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/isolate="healthy individual"
/db.xref="taxon:9606"
/chromosome="10"
/map="10q24.1 or 10q23"
/clone="pCR TM 11-Fas delta(3,4,6)"
/cell_type="peripheral blood mononuclear cells"
391..762
/gene="Fas/Apo-1"
391..637
/gene="Fas/Apo-1"
/notes="3 and 4"
700..762
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/number=6
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.7e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||
Db 286 AAGAGAAAGGAGTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCAT 345
   |||||

QY 61 GAATCTCCAACCTTAATCTGGAACAGTGCATCAATATTTATCTGATGTTGACTTGAGT 120
   |||||
Db 346 GAATCTCCAACCTTAATCTGGAACAGTGCATCAATATTTATCTGATGTTGACTTGAGT 405
   |||||

QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 180
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Db 406 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 465
   |||||

QY 181 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 240
   |||||
Db 466 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 525
   |||||

QY 241 GCAGAACAGAAAGTTCAACTGCTCTGTAATGGCATCAACTTCATGGAAGAAAGAGCG 300
   |||||
Db 526 GCAGAACAGAAAGTTCAACTGCTCTGTAATGGCATCAACTTCATGGAAGAAAGAGCG 585
   |||||

QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAAATT 360
   |||||
Db 586 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAAATT 645
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QY 361 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 420
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Db 646 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 705
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QY 421 ATCCAAAGCTTGGTC 435
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Db 706 ATCCAAAGCTTGGTC 720
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RESULT 5
HSFAS4DEL
LOCUS
DEFINITION H.sapiens Fas/Apo 1 mRNA for Fas soluble protein (clone FAS
Exo4Del).
ACCESSION 270519
VERSION 270519.1 GI:1418817
KEYWORDS FAS soluble protein; Fas/Apo 1 gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 899)
AUTHORS Papoff, G., Cascino, I., Eramo, A., Starace, G., Lynch, D.H. and
Ruberti, G.
TITLE A N-terminal domain shared by Fas soluble variants prevents cell
death in vitro
JOURNAL J. Immunol. (1996), In press
REFERENCE 2 (bases 1 to 899)

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AUTHORS Ruberti G.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R., Immunology, viale C.Marx 43, Rome, Italy, I-00137
FEATURES Location/Qualifiers
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/isolate="LN"
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CDS 1..450
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exon 31..196
/number=2
/evidence=experimental
exon 197..334
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/evidence=experimental
exon 335..396
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exon 397..459
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exon 460..542
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exon 543..567
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exon 568..899
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BASE COUNT 307 a 179 c 197 g 216 t
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Best Local Similarity 100.0%; Pred. No. 9.7e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGACAGAGAAAGAAACCAAGGTTCTCAT 60
Db 462 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGACAGAGAAAGAAACCAAGGTTCTCAT 521
QY 61 GAATCTCCACCTTAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
Db 522 GAATCTCCACCTTAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 581
QY 121 AAATATATACCACTATTCTGTCAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGA 180
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Db 582 AAATATATACCACTATTCTGTCAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGA 641
QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAATGACAAATGTCCAAGACACA 240
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Db 642 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAATGACAAATGTCCAAGACACA 701
QY 241 GCAGAACACAGAAAGTCAACTGCTTCTGTAATTTGGCATCAACTTCATCGAAGAAAGCG 300
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Db 702 GCAGAACACAGAAAGTCAACTGCTTCTGTAATTTGGCATCAACTTCATCGAAGAAAGCG 761
QY 301 TATGACACATTTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTCAGAGAAAAT 360
|||||
Db 762 TATGACACATTTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTCAGAGAAAAT 821
QY 361 CAGACATATCATCTCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAAATGAA 420
|||||
Db 822 CAGACATATCATCTCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAAATGAA 881
QY 421 ATCCAAAGCTTGTC 435
Db 882 ATCCAAAGCTTGTC 896
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RESULT 6
HSFAS34
LOCUS H.sapiens mRNA for Fas/Apo-1 (clone pCMTM1-Fasdelta(3,4)).
DEFINITION X83490
ACCESSION X83490.1
VERSION GI:971454
KEYWORDS FAS gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 920)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Cheng, J., Zhou, T., Liu, C., Shapiro, J.P., Brauer, M.J., Kiefer, M.C., Bart, P.J., and Mountz, J.D.
Protection from Fas-mediated apoptosis by a soluble form of the Fas molecule
Science 263 (5154), 1759-1762 (1994)
94182136
PUBMED 7510905
REFERENCE 2 (bases 1 to 920)
AUTHORS Cheng, J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) J. Cheng, University of Alabama at Birmingham, Division of Clinical Immunol. & Rheum., UAB Station, LHRB 473, Birmingham AL 35294-0007, USA
3 (bases 1 to 920)
Liu, C., Cheng, J., and Mountz, J.D.
Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation.
Biochem. J. 310 (Pt 3), 957-961 (1995)
96013198
PUBMED 7575433
COMMENT Related sequences: M67454 and X63717.
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.6e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 60
DB 349 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 408
QY 61 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 120
DB 409 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 468
QY 121 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 180
DB 469 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 528
QY 181 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 240
DB 529 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 588
QY 241 GCAGAACAGAAAGTTCACCTGCTTAATGGCATCACTTCAATGGCAAGAAAGAGCG 300
DB 589 GCAGAACAGAAAGTTCACCTGCTTAATGGCATCACTTCAATGGCAAGAAAGAGCG 648
QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAATTT 360
DB 649 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAATTT 708
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTACTGATGATGATGATGATGATGATGATGATGAT 420
DB 709 CAGACTATCATCTCAAGGACATTTACTAGTACTGATGATGATGATGATGATGATGATGATGAT 768
QY 421 ATCCAAAGCTTGGTC 435
DB 769 ATCCAAAGCTTGGTC 783

RESULT 7
HSPASCDL1
LOCUS HSPASCDL1 945 bp mRNA linear PRI 15-DEC-1997
DEFINITION H. sapiens FASTM Del mRNA.
ACCESSION 247993
VERSION 247993.1 GI:728578
KEYWORDS FAS gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ruberti, G.
Direct Submission
Submitted (24-JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,
Immunology, viale C. Merz 43, Rome, Italy, I-00137
Three functional soluble forms of the human apoptosis-inducing Fas
molecule are produced by alternative splicing
J. Immunol. 154 (6), 2706-2711 (1995)
5181785
PUBMED 753181
COMMENT On Mar 25, 1995 this sequence version replaced gi:695538.
FEATURES
Location/Qualifiers
1..945
/organism="Homo sapiens"
/isolate="GF"
/db_xref="taxon:9606"
/chromosome="10"
/clone="FASTM Del"
/cell_type="PHA-activated PBMC"
1..945
/standard_name="FAS/Apo 1"
/note="Alternative splicing variant of FAS gene missing
exon 6"

CDS
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/evidence=experimental
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/db_xref="SPTREMBL:Q14293"
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Best Local Similarity 100.0%; Pred. No. 9.6e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 60
DB 508 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 567
QY 61 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 120
DB 568 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 627
QY 121 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 180
DB 628 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 587
QY 181 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 240
DB 688 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 747
QY 241 GCAGAACAGAAAGTTCACCTGCTTAATGGCATCACTTCAATGGCAAGAAAGAGCG 300
DB 748 GCAGAACAGAAAGTTCACCTGCTTAATGGCATCACTTCAATGGCAAGAAAGAGCG 807
QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAATTT 360
DB 769 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAATTT 807
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Db 808 TATGACACATTGATTAAAGATCTCAAAAGACCAATCTTTGTACTCTTCAGAGAAATTT 867
 QY 361 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 420
 Db 868 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 927
 QY 421 ATCCAAAGCTTGCTC 435
 Db 928 ATCCAAAGCTTGCTC 942

RESULT 8

E05336
 LOCUS E05336 1008 bp RNA linear PAT 29-SEP-1997
 DEFINITION DNA encoding human Fas protein.
 ACCESSION E05336
 VERSION E05336.1 GI:2173525
 KEYWORDS JP 1993219959-A/2.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1008)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Osada,J.
 TITLE NEW DNA AND PROTEIN CODES THEREWITH
 JOURNAL Patent: JP 1993219959-A/2 31-AUG-1993;

COMMENT OSAKA BIO SCI-KENKYUSHO
 OS Homo sapiens (human)
 PN JP 1993219959-A/2
 PD 31-AUG-1993
 PI 12-FEB-1992 JP 992028090

PC C12N15/12.C07K13/00.C12P21/02;
 CC strandedness: Double;
 CC topology: Linear;
 CC *source: cell_line=KT-3;
 FH Key Location/Qualifiers

FT CDS 1..1008
 FT /product="Fas protein".

FEATURES
 source 1..1008
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 343 a 205 c 217 g 243 t

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 9.6e-89;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAGTACAGAAACATCGAGAAAGCACAGAAAGAAACCAAGGTTCTCAT 60
 Db 571 AAGAGAAAGGAAGTACAGAAACATCGAGAAAGCACAGAAAGAAACCAAGGTTCTCAT 630
 QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
 Db 631 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 690
 QY 121 AAATATATCACCACATTTCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA 180
 Db 691 AAATATATCACCACATTTCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA 750
 QY 181 AAGATGGTGTCAATGAAGCCAAATAGATGACATCAAGAAATGACAAATGTCCAAGACACA 240
 Db 751 AAGATGGTGTCAATGAAGCCAAATAGATGACATCAAGAAATGACAAATGTCCAAGACACA 810
 QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTCATGGAAGAAAGAACGC 300
 Db 811 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTCATGGAAGAAAGAACGC 870
 QY 301 TATGACACATTTGATTAAGATCTCAAAAGACCAATCTTTGTACTCTTCAGAGAAATTT 360

Db 871 TATGACACATTTGATTAAGATCTCAAAAGACCAATCTTTGTACTCTTCAGAGAAATTT 930
 QY 361 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 420
 Db 931 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 990
 QY 421 ATCCAAAGCTTGCTC 435
 Db 991 ATCCAAAGCTTGCTC 1005

RESULT 9

HSFAS6
 LOCUS HSFAS6 1104 bp mRNA linear PRI 28-NOV-1995
 DEFINITION H.sapiens mRNA for Fas/Apo-1 (clone pCMT11-FasdeltaTM).
 ACCESSION X83493
 VERSION X83493.1 GI:971457
 KEYWORDS FAS gene.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1104)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Cheng,J., Zhou,T., Liu,C., Shapero,J.P., Brauer,M.J., Kiefer,M.C.,
 Bart,P.J. and Mountz,J.D.
 TITLE Protection from Fas-mediated apoptosis by a soluble form of the Fas
 molecule

JOURNAL Science 263 (5154), 1759-1762 (1994)
 MEDLINE 94182136
 PUBMED 7510905

REFERENCE 2 (bases 1 to 1104)
 Cheng,J.
 TITLE Direct Submission

JOURNAL Submitted (14-DEC-1994) J. Cheng, University of Alabama at
 Birmingham, Division of Clinical Immunol. & Rheum., UAB Station,
 LHRB 473; Birmingham AL 35294-0007, USA

REFERENCE 3 (bases 1 to 1104)
 Liu,C., Cheng,J. and Mountz,J.D.
 TITLE Differential expression of human Fas mRNA species upon peripheral
 blood mononuclear cell activation

JOURNAL Biochem. J. 310 (Pt 3), 957-963 (1995)
 MEDLINE 96013198
 PUBMED 7575433

COMMENT Related sequences: M67454 and X63717.
 FEATURES
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 Location/Qualifiers
 /organism="Homo sapiens"
 /isolate="healthy individual"
 /db_xref="taxon:9606"
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 /number=6
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BASE COUNT 384 a 218 c 233 g 269 t

ORIGIN
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 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
 Db 593 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 652

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		Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	880	AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAAAACCAAGGTTCTCAT 939
OY	61	GAATCTCCACCTTAATCTCTGAACAGTGGCAATAATTTATCTGATGTGACTTGAGT 120
Db	940	GAATCTCCACCTTAATCTCTGAACAGTGGCAATAATTTATCTGATGTGACTTGAGT 999
OY	121	AAATATATACCACTATTGCTGGAGTCATGACACTAAAGGTTGTTGTCGA 180

[illegible]

||||| 1062 CAGACTATCTCTCAGGACATCTAGTACTGAGTCTCAGAAATTCAGAAATGAA 1121
Db
QY 421 ATCCAAAGCTTGTC 435
Db 1122 ATCCAAAGCTTGTC 1136
RESULT 12
LOCUS I63530 2471 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 18 from patent US 5663070.
ACCESSION I63530
VERSION I63530.1 GI:2481103
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2471)
AUTHORS Barr, P.J., Shapiro, J.P. and Kiefer, M.C.
TITLE Recombinant production of a soluble splice variant of the Fas (Apo-1) antigen, Fas TM
JOURNAL Patent: US 5663070-A 18 02-SEP-1997
FEATURES Location/Qualifiers
source 1..2471
BASE COUNT 807 a 474 c 489 g 701 t
ORIGIN
Query Match 100.0%; Score 435; DB 6; Length 2471;
Best Local Similarity 100.0%; Pred. No. 9e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 702 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGTTCTCAT 761
QY 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
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QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 180
Db 822 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 881
QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAGACACA 240
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QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTGTACTCTTGACAGAAATTT 360
Db 1002 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTGTACTCTTGACAGAAATTT 1061
QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTTCAAACCTTCAGAAATGAA 420
Db 1062 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTTCAAACCTTCAGAAATGAA 1121
QY 421 ATCCAAAGCTTGTC 435
Db 1122 ATCCAAAGCTTGTC 1136
RESULT 13
LOCUS A87646 2534 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 4 from Patent W09835692.
ACCESSION A87646
VERSION A87646.1 GI:6736281
KEYWORDS

unidentified.
unclassified.
unclassified.
REFERENCE 1 (bases 1 to 2534)
AUTHORS Scream, G.R. and Xu, X.
TITLE MATERIALS AND METHODS RELATING TO THE PROTECTION OF USEFUL IMMUNE CELLS
JOURNAL Patent: WO 9835692-A 4 20-MUG-1998;
SCREATOR GAVIN ROBERT (GB); ISIS INNOVATION (GB)
FEATURES Location/Qualifiers
source 1..2534
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 817 a 487 c 503 g 727 t
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Best Local Similarity 100.0%; Pred. No. 9e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGTTCTCAT 60
Db 765 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGTTCTCAT 824
QY 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
Db 825 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 884
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 180
Db 885 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 944
QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAGACACA 240
Db 945 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAGACACA 1004
QY 241 GCAGAACAGAAAGTTCACCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 300
Db 1005 GCAGAACAGAAAGTTCACCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 1064
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTGTACTCTTGACAGAAATTT 360
Db 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTGTACTCTTGACAGAAATTT 1124
QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTTCAAACCTTCAGAAATGAA 420
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QY 421 ATCCAAAGCTTGTC 435
Db 1185 ATCCAAAGCTTGTC 1199
RESULT 14
LOCUS AR163572 2534 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270998.
ACCESSION AR163572
VERSION AR163572.1 GI:16234218
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2534)
AUTHORS Nagata, S., Itoh, N. and Yonehara, S.
TITLE DNA coding for human cell surface antigen
JOURNAL Patent: US 6270998-A 1 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..2534
/organism="unknown"
BASE COUNT 817 a 487 c 503 g 727 t
ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 18:18:33 ; Search time: 217 Seconds
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Title: US-09-884-987-1_COPY_765_1199

Perfect score: 435

Sequence: 1 aagagaagaagtagacagaa.....atgaatccaaagttagtc 435

Scoring table: IDENTITY_NUC

Gapop 10.0., Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435	100.0	836	24	Sequence #9 used t
2	435	100.0	920	17	Human Fas soluble
3	435	100.0	920	24	Human cDNA differe
4	435	100.0	1104	17	Human Fas soluble
5	435	100.0	1167	17	Human Fas antigen
6	435	100.0	1457	21	Apoptobody3sc fusi
7	435	100.0	2471	16	Fas-delta-TM cDNA
8	435	100.0	2471	20	Soluble Fas recept
9	435	100.0	2534	13	Human cell surface

10 435 100.0 2534 16 AAQ95297
11 435 100.0 2534 17 AAT16303
12 435 100.0 2534 18 AAV07002
13 435 100.0 2534 19 AAV32993
14 435 100.0 2551 21 AAC61798
15 435 100.0 2551 24 ABN79588
16 435 100.0 8282 21 AA234938
17 435 100.0 8282 22 AAF30947
18 435 100.0 8345 21 AA234939
19 435 100.0 8345 22 AAF30948
20 433.4 99.6 857 17 AAT34530
21 433.4 99.6 1468 22 AAA91129
22 433.4 99.6 1483 22 AAA91130
23 433.4 99.6 3009 22 AAA91131
24 433.4 99.6 3009 22 AAA91132
25 394.4 90.7 398 24 ABL79512
26 383.6 88.2 460 24 ABL80178
27 354 81.4 975 17 AAT34528
28 354 81.4 975 24 ABL63728
29 354 81.4 975 24 ABL68887
30 330 75.9 1840 24 ABN79684
31 167.6 38.5 984 14 AAC61859
32 167.6 38.5 1480 21 ABN79649
33 167.6 38.5 1480 24 ABN79649
34 167.6 38.5 1506 16 AAQ95302
35 167.6 38.5 1506 17 AAT16305
36 167.6 38.5 1506 20 AAV71961
37 83.4 19.2 338 24 ABN79682
38 60 13.8 60 24 ABN40425
39 60 13.8 60 24 ABN58759
40 60 13.8 60 24 ABN58760
41 60 13.8 60 24 ABN58963
42 43 9.9 1956 18 AAT67161
C 43 41.6 9.6 12177 24 ABL32650
C 44 39.8 9.1 7449 24 ABL32276
45 39.6 9.1 882 24 ABN70783

ALIGNMENTS

RESULT 1

ABN79685
ID ABN79685 standard; DNA; 836 bp.

XX AC ABN79685;

XX DT 29-JUL-2002 (first entry)

DE Sequence #9 used to generate target oligonucleotides.

XX Human; immunosuppressive; antiinflammatory; hepatotropic;

KW cytostatic; vasotropic; hepatitis; cancer; allograft rejection;

KW ds; Fas.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..399

FT /tag= a

FT /product= "protein encoded by sequence

FT used create target oligonucleotides"

XX US2002004490-A1.

XX 10-JAN-2002.

XX 09-MAR-2001; 2001US-0802669.

XX 12-APR-1999; 99US-0290640.

PR 18-SEP-2000; 2000US-0665615.

XX (DEAN/) DEAN N M.

PA

PA (MARC/) MARCUSSEON E. G.
 PA (WYAT/) WYATT J.
 PA (ZHAN/) ZHANG H.

XX Dean NM, Marcussoson EG, Wyatt J, Zhang H;
 XX

DR WPI: 2002-204886/26.
 DR P-PSDB: ABP35574.

XX Novel antisense compound targeted to nucleic acid encoding Fas, Fas
 PT ligand or Fas associated protein-1 is useful for inhibiting expression
 PT of Fas, Fas ligand, or Fas-1 in cells or tissues, and for treating
 PT hepatitis

XX Example 18: Page 67-68; 84pp; English.

XX This invention relates to an antisense compound encoding Fas,
 CC Fas ligand, or Fas associated protein-1 (Fap-1). The inhibition of
 CC Fas mediated signalling is thought to be immunosuppressive,
 CC antiinflammatory, hepatotropic, cytostatic and vasotropic.
 CC Antisense oligonucleotides were designed to target human Fas.
 CC Oligonucleotides were synthesized as chimeric oligonucleotides
 CC and are useful for treating an animal having an autoimmune or
 CC inflammatory disease e.g., hepatitis, cancer, a condition associated
 CC with apoptosis, allograft rejection, or ischemia reperfusion
 CC injury. Optionally, the above mentioned conditions are prevented by
 CC contacting the allograft with the antisense oligonucleotide. The
 CC oligonucleotides are used in diagnostics, therapeutics, prophylaxis,
 CC and as research reagents and in kits. The oligonucleotides are also
 CC useful for research purposes. The present nucleotide sequence is
 CC related to human Fas.

XX Sequence 836 BP; 297 A; 166 C; 183 G; 190 T; 0 other;

Query Match 100.0%; Score 435; DB 24; Length 836;
 Best Local Similarity 100.0%; Pred. No. 1.9e-108;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60
 DB 399 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 458
 QY 61 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGTGAGTTGAGT 120
 DB 459 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGTGAGTTGAGT 518
 QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGA 180
 DB 519 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGA 578
 QY 181 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCACAGACACA 240
 DB 579 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATGACAAATGTCACAGACACA 638
 QY 241 GCAGAACAGAAAGTCAACTTCTGCTGTAATTTGGCATCAACTTCATGGAAAGAAAGAGCG 300
 DB 639 GCAGAACAGAAAGTCAACTTCTGCTGTAATTTGGCATCAACTTCATGGAAAGAAAGAGCG 698
 QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAACTTTGTTACTCTTTCAGAGAAATTT 360
 DB 699 TATGACACATTTGATTAAGATCTCAAAAAGCCAACTTTGTTACTCTTTCAGAGAAATTT 758
 QY 361 CAGACTATCATCTCAAGGACATTAAGTACTGAGTCAAGAAATTTCAAACTTCAGAAATGAA 420
 DB 759 CAGACTATCATCTCAAGGACATTAAGTACTGAGTCAAGAAATTTCAAACTTCAGAAATGAA 818
 QY 421 ATCCAAAGCTTTGGTC 435
 DB 819 ATCCAAAGCTTTGGTC 833

RESULT 2
 AAT34529

ID

XX

AC

XX

XX

DT

DE

XX

XX

KW

KW

XX

OS

XX

FH

FT

CDS

FT

sig_peptide

FT

mat_peptide

FT

XX

XX

PN

XX

PD

XX

XX

PF

XX

XX

PR

XX

XX

PA

XX

XX

PI

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DR

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PT

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PT

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AAT34529 standard; cDNA: 920 BP.

AAT34529;

10-OCT-1996 (first entry)

Human Fas soluble antigen Fas del3 CDNA.

Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
 angioimmunoblastic lymphadenopathy; AILD; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 26...307

sig_peptide /tag= a

FT 26...73

mat_peptide /tag= b

FT 74...304

mat_peptide /tag= c

WO9620206-A1.

04-JUL-1996.

22-DEC-1995; 95WO-US17083.

23-DEC-1994; 94US-0371263.

(UABR-) UAB RES FOUND.

Cheng J, Liu C, Mountz JD, Zhou T;

WPI: 1996-321796/32.

P-PSDB; AAR9684.

Natural, soluble form of Fas antigen secreted by human cells is

result of alternative mRNA processing - used to diagnose

Fas-associated disease, e.g. systemic lupus erythematosus

Disclosure: Page 121-122; 152pp; English.

4 Human Fas cDNA variants (AAT34527-30) are derived from alternative

splicing of Fas gene transcripts. They were identified following

PCR amplification of cDNA derived from the peripheral blood

mononuclear cells of systemic lupus erythematosus (SLE) and

angioimmunoblastic lymphadenopathy (AILD) patients and from healthy

subjects. In comparison to the Fas gene (AAT34526), variant Fas del3

(AAT34529) has a deletion of nucleotides 391-637. This deletion causes

frame shifting and an altered amino acid sequence (AAR9683).

Sequence 920 BP; 312 A; 180 C; 186 G; 242 T; 0 other;

Query Match 100.0%; Score 435; DB 17; Length 920;

Best Local Similarity 100.0%; Pred. No. 1.9e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60

DB 349 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 408

QY 61 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGTGAGTTGAGT 120

DB 409 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGTGAGTTGAGT 468

QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGA 180

DB 469 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGA 528

QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGTCACAGACACA 240

DB 529 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGTCACAGACACA 588

241	QY	GCAGAACAGAAAGTTCTA	CTGCTCGTAAATGGCATCA	CACTTCATGTGAAAGAAAGCG	300
589	Db	GCAGAACAGAAAGTTCA	ACTGCTTCGTAATTTGGCAT	CAACTTTCATGTGAAAGAAAGCG	648
301	QY	TATGACACATGATTAA	GATCTCAGAAAAGCCCAAT	CTTTGTACTCTTCGAGAGAAAT	360
649	Db	TATGACACATGATTAA	GATCTCAGAAAAGCCCAAT	CTTTGTACTCTTCGAGAGAAAT	708
361	QY	CAGACTATCATCTCTC	CAAGGACATTACTAGTGACT	TCAGAAAATTCAGAAATGAA	420
709	Db	CAGACTATCATCTCTC	CAAGGACATTACTAGTGACT	TCAGAAAATTCAGAAATGAA	768
421	QY	ATCCAAAGCTTGGTC	435		
769	Db	ATCCAAAGCTTGGTC	783		

RESULT 3

ABK84693
ID ABK84693 standard; cDNA: 920 BP.

the level of expression of the gene is indicative of inflammation;
(4) treating (M5) an inflammation (especially chronic) or in a tissue,
an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
inflammation with an agent that modulates the expression of gene(s)
from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
modulating GA; M3 is useful for screening an agent capable of modulating
GCA preferably in an inflammation in a tissue; M4 is useful for
detecting an inflammation (especially chronic) in a tissue, an allergic
response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
reperfusion injury, ARDS, adult respiratory distress syndrome,
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
peritonatal disease; also bacterial infection, viral infection, and
parasitic infection, protozoal infection, fungal infection and M5 is
useful for treating one of the above conditions. The present
sequence represents a gene differentially expressed in granulocytes.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

RESULT 4
AAT34527

AA134527
ID AAT34527 standard: CDNA: 1104 BP.

XX Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
KW

angioimmunoblastic lymphadenopathy; AILD; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 26..970

XX FT sig_peptide /*tag= a

XX FT mat_peptide /*tag= b

XX FT /*tag= c

XX PN W09620206-A1.

XX PD 04-JUL-1996.

XX PF 22-DEC-1995; 95WO-US17083.

XX PR 23-DEC-1994; 94US-0371263.

XX PA (UABR-) UAB RES FOUND.

XX PI Cheng J, Liu C, Mountz JD, Zhou T;

XX DR WPI; 1996-321796/32.

XX DR P-PSDB; AAR99682.

XX PT Natural, soluble form of Fas antigen secreted by human cells is

XX PT result of alternative mRNA processing - used to diagnose

XX PT Fas-associated disease, e.g. systemic lupus erythematosus

XX PS Disclosure; Page 112-113; 152pp; English.

XX CC 4 Human Fas cDNA variants (AAT34527-30) are derived from alternative

XX CC splicing of Fas gene transcripts. They were identified following

XX CC PCR amplification of cDNA derived from the peripheral blood

XX CC mononuclear cells of systemic lupus erythematosus (SLE) and

XX CC angioimmunoblastic lymphadenopathy (AILD) patients and from healthy

XX CC subjects. In comparison to the Fas gene (AAT34526), variant Fas dell

XX CC (AAT34528) lacks nucleotides 700-762 as a result of an exon deletion.

XX CC The encoded protein (AAR99682) lacks the transmembrane region of

XX CC insoluble Fas antigen (AAR99681). The cDNA can be used for prodn. of

XX CC recombinant, soluble dell variant or as a specific probe.

XX SQ Sequence 1104 BP; 384 A; 218 C; 233 G; 269 T; 0 other;

Query Match 100.0%; Score 435; DB 17; Length 1104;

Best Local Similarity 100.0%; Pred. No. 2e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGCAAGGTTCTCAT 60

DB 533 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGCAAGGTTCTCAT 592

QY 61 GAATCTCCAACCTTAATCTGGAACAGTGGCAATTAATTTATCTGATGTTGACCTGAGT 120

DB 593 GAATCTCCAACCTTAATCTGGAACAGTGGCAATTAATTTATCTGATGTTGACCTGAGT 652

QY 121 AATATATACACCACTATTGCTGGAGTATGACACTAAGTCAAGTTAAAGGTTGTTGCA 180

DB 653 AATATATACACCACTATTGCTGGAGTATGACACTAAGTCAAGTTAAAGGTTGTTGCA 712

QY 181 AAGATGTGTCAATGAAGCCAAATATAGATGATCAAGATGCAATGTCACACACA 240

DB 713 AAGATGTGTCAATGAAGCCAAATATAGATGATCAAGATGCAATGTCACACACA 772

QY 241 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCACTTCATGGAAGAAAGAACGCG 300

DB 773 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCACTTCATGGAAGAAAGAACGCG 832

QY 301 TATGACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCGACAGAAAT 360

DB 833 TATGACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCGACAGAAAT 892

QY 361 CAGACTATCATCTCTAAGGACATTTACTAGTCTCAGAAAAATTCAGAAATGAA 420

DB 893 CAGACTATCATCTCTAAGGACATTTACTAGTCTCAGAAAAATTCAGAAATGAA 952

QY 421 ATCCAAAGCTTGGTC 435

DB 953 ATCCAAAGCTTGGTC 967

RESULT 5

AAT34526

ID AAT34526 standard; cDNA; 1167 BP.

XX AC AAT34526;

XX DT 10-OCT-1996 (first entry)

XX DE Human Fas antigen cDNA.

XX KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;

XX KW angioimmunoblastic lymphadenopathy; AILD; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 26..1033

XX FT sig_peptide /*tag= a

XX FT /*tag= b

XX FT mat_peptide 74..1030

XX FT /*tag= c

XX PN W09620206-A1.

XX PD 04-JUL-1996.

XX PF 22-DEC-1995; 95WO-US17083.

XX PR 23-DEC-1994; 94US-0371263.

XX PA (UABR-) UAB RES FOUND.

XX PI Cheng J, Liu C, Mountz JD, Zhou T;

XX DR WPI; 1996-321796/32.

XX DR P-PSDB; AAR99681.

XX PT Natural, soluble form of Fas antigen secreted by human cells is

XX PT result of alternative mRNA processing - used to diagnose

XX PT Fas-associated disease, e.g. systemic lupus erythematosus

XX PS Disclosure; Page 107-108; 152pp; English.

XX CC A cDNA clone (AAT34526) codes for a membrane receptor-like protein,

XX CC Fas antigen (AAR99681). It was isolated from cDNA derived from the

XX CC peripheral blood mononuclear cells of systemic lupus erythematosus

XX CC (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients, and

XX CC from healthy subjects, by PCR amplification. In addition to fas

XX CC cDNA, 4 other PCR products were obt'd. (see also AAT34527-30). These

XX CC coded for soluble forms (AAR99682-85) of Fas antigen that are present

XX CC at higher levels in SLE and AILD patients than the non-soluble Fas

XX CC antigen.

XX SQ Sequence 1167 BP; 394 A; 231 C; 247 G; 295 T; 0 other;

Query Match 100.0%; Score 435; DB 17; Length 1167;

Best Local Similarity 100.0%; Pred. No. 2e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGCAAGGTTCTCAT 60

DB 596 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGCAAGGTTCTCAT 655

Qy	61	GAATCTCCAACCTTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT	120
Db	656	GAATCTCCAACCTTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT	715
Qy	121	AAATATATACCACTATTGCTGGAGTCATGACACTAAGCTTAAGGCTTTGTTCGA	180
Db	716	AAATATATACCACTATTGCTGGAGTCATGACACTAAGCTTAAGGCTTTGTTCGA	775
Qy	181	AAGAATGGTCTCAATGAAGCCAAATAGATGAGATCAAGAATGACAAATGTCCAAGACACA	240
Db	776	AAGAATGGTCTCAATGAAGCCAAATAGATGAGATCAAGAATGACAAATGTCCAAGACACA	835
Qy	241	CGAAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCATGAAAGAAAGAAGCG	300
Db	836	CGAAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCATGAAAGAAAGAAGCG	895
Qy	301	TATGACACATTTGATTAAAGATCTCAAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAAAATT	360
Db	896	TATGACACATTTGATTAAAGATCTCAAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAAAATT	955
Qy	361	CAGACTATCATCTCAAGGACATTACTAGTGACTCAGAAAAATTCAAACTTTCAGAAATGAA	420
Db	956	CAGACTATCATCTCAAGGACATTACTAGTGACTCAGAAAAATTCAAACTTTCAGAAATGAA	1015
Qy	421	ATCCAAAGCTTGGTC	435
Db	1016	ATCCAAAGCTTGGTC	1030

RESULT 6	
AAA39167	
ID	AAA39167 standard; DNA; 1457 BP.
XX	
XX	
AC	AAA39167;
XX	
XX	
DT	05-SEP-2000 (first entry)
XX	
DE	Apoptobody3sc fusion protein encoding nucleotide sequence SEQ ID NO:7.
XX	
KW	Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
KW	medical; pharmaceutical; pharmacological; biochemical; ds.
XX	
XX	
OS	Homo sapiens.
OS	Synthetic.

XX JP2000102389-A.
 XX
 XX 11-APR-2000.
 XX
 XX 29-SEP-1998; 98JP-0291441.
 XX
 XX 29-SEP-1998; 98JP-0291441.
 XX
 XX (HAGI/) HAGIWARA Y.
 XX (HAGI/) HAGIWARA H.
 XX
 XX
 XX WPI: 2000-332085/29.
 XX P-PSDB: AAY91029.
 XX
 XX
 XX Causing apoptosis comprises transfecting fused gene to cell and
 XX reacting cell with idiotypic antibody -
 XX
 XX Disclosure; Page 7; 10pp; Japanese.
 XX PS

CC	transfected to a cell to express the fused gene and then an idlotype
CC	antibody is reacted with the expressed cell. The method is useful in
CC	medical, pharmaceutical, pharmacological and biochemical fields. The
CC	present sequence encodes a fusion protein designated apoptobody3sc,
CC	which is used in the exemplification of the present invention.
XX	
SQ	Sequence 1457-BP; 441 A; 309 C; 340 G; 367 T; 0 other;
	Query Match 100.0%; Score 435; DB 21; Length 1457;
	Best Local Similarity 100.0%; Pred. No. 2.2e-108;
	Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 AAGAGAAGCAGTACAGAAACATCGAAGAACACAGACAGGAAGAAACCAGGTTCTCAT 60
Dd	880 AAGAGAAGGAGGTACGAAAACAATGCAGAAAGCACAGAAGGAAACCAGGTTCTCAT 939
Qy	61 GAATCTCCAACCTTAATCTCGAAACAGTGCGCAATAAATTATCTGATGTGACTTGAGT 120
Dd	940 GAATCTCCAACCTTAATCTCGAAACAGTGCGCAATAAATTATCTGATGTGACTTGAGT 999
Qy	121 AAATATATACACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGA 180
Dd	1000 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGA 1059
Qy	181 AAGAAATCGTGTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAGACACA 240
Dd	1060 AAGAAATCGTGTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAGACACA 1119
Qy	241 CGAAGACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGAAAGAAGAAGCG 300
Dd	1120 GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATGAAAGAAGAAGCG 1179
Qy	301 TAIGACACATTGATTAAGATCTCAAAAAAGGCCAATCTTTGTACTCTTGACGAGAAAAATT 360
Dd	1180 TAIGACACATTGATTAAGATCTCAAAAAAGGCCAATCTTTGTACTCTTGACGAGAAAAATT 1239
Qy	361 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAAATTCAAACACTTCAGAAATGAA 420
Dd	1240 CAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAAATTCAAACTTCAGAAATGAA 1299
Qy	421 ATCCAAAGCTTTGGTC 435
Dd	1300 ATCCAAAGCTTTGGTC 1314

RESULT	7
AAQ93879	
ID	AAQ93879 standard; cDNA; 2471 BP.
XX	
AC	AAQ93879;
XX	
DT	06-NOV-1995 (first entry)
XX	
DE	Fas-delta-TM cDNA.
XX	
KW	Fas-delta-TM; Transmembrane deletion; apoptosis; antibody;
KW	adoptive immunotherapy; transgenic animal; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 195..1139
FT	*tag= a
FT	sig_peptide 195..242
FT	/tag= b
FT	mat_peptide 243..1136
FT	/tag= c
XX	
PX	WO9513701-A.
PN	
XX	
PD	26-MAY-1995.
PF	15-NOV-1994. 94WO-US13173.

QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 180
Db 822 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 881
QY 181 AGAATGGTGTCAATGAAGCCAAATAGATGACATCAAGATGACAAATGTCCAGACACA 240
Db 882 AGAATGGTGTCAATGAAGCCAAATAGATGACATCAAGATGACAAATGTCCAGACACA 941
QY 241 GCAGACAGAAATCTCACTGCTTCTGTAATTTGGCATCAACTTCAATGGAAGAAAGAGCG 300
Db 942 GCAGACAGAAATCTCACTGCTTCTGTAATTTGGCATCAACTTCAATGGAAGAAAGAGCG 1001
QY 301 TATGACACATTTGTAATGAAGATCTCAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 360
Db 1002 TATGACACATTTGTAATGAAGATCTCAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 1061
QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 420
Db 1062 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 1121
QY 421 ATCCAAAGCTTGGTC 435
Db 1122 ATCCAAAGCTTGGTC 1136

RESULT 9

AAQ29959
ID AAQ29959 standard; cDNA to mRNA; 2534 BP.

XX AC AAQ29959;

XX 12-MAR-1993 (first entry)

XX Human cell surface antigen.

XX Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT sig_peptide 195..242

FT mat_peptide 243..1199

FT conflict 1046

FT polyA_signal 1831..1836

FT polyA_signal 2352..2357

FT polyA_signal 2518..2523

FT note- "this residue is not present in pF3"

FT polyA_signal 1831..1836

FT polyA_signal 2352..2357

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

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FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

FT polyA_signal 2518..2523

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Claim 3; Fig 1 and 2; 27pp; English.

A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The cDNA was ligated to BstXI-cut vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-7 cells which were then suspended in buffer containing murine anti-Fas Ab. The cells were "panned" on plates pre-coated with goat anti-mouse antibodies. The Fas-expressing cells adhered to the plates. Extrachromosomal DNA was prepared from adhered cells and used to transform E.coli WMI00 cells. A 520bp XhoI-BamHI fragment from a positive clone (pF3) was used to screen the KT-3 cDNA library. The longest cDNA clone was designated pF58 and contains an ORF corresp. to a 335 amino acid pre-protein and a 319 amino acid mature protein (i.e. human Fas antigen).

Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 13; Length 2534;

Best Local Similarity 100.0%; Pred. No. 2.6e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGAAAGGAAGTACAGAAACATGCAGAAACGACAGAAAGGAAACCAAGTTCTCAT 60

Db 765 AGAGAAAGGAAGTACAGAAACATGCAGAAACGACAGAAAGGAAACCAAGTTCTCAT 824

QY 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTCAGT 120

Db 825 GAATCTCCACCTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTCAGT 884

QY 121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 180

Db 885 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 944

QY 181 AGAATGGTGTCAATGAAGCCAAATAGATGACATCAAGATGACAAATGTCCAGACACA 240

Db 945 AGAATGGTGTCAATGAAGCCAAATAGATGACATCAAGATGACAAATGTCCAGACACA 1004

QY 241 GCAGACAGAAATCTCACTGCTTCTGTAATTTGGCATCAACTTCAATGGAAGAAAGAGCG 300

Db 1005 GCAGACAGAAATCTCACTGCTTCTGTAATTTGGCATCAACTTCAATGGAAGAAAGAGCG 1064

QY 301 TATGACACATTTGTAATGAAGATCTCAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 360

Db 1065 TATGACACATTTGTAATGAAGATCTCAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 1124

QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 420

Db 1125 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 1184

QY 421 ATCCAAAGCTTGGTC 435

Db 1185 ATCCAAAGCTTGGTC 1199

RESULT 10

AAQ95297

ID AAQ95297 standard; cDNA; 2534 BP.

XX AC AAQ95297;

XX 19-FEB-1996 (first entry)

XX Plasmid pF58 contg. human Fas cDNA.

XX Plasmid pF58; human Fas cDNA; soluble membrane protein;

XX antibody production; diseases; treatment; prevention; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 195..1202

FT tag= a

FT tag= a

FT tag= a

FT tag= a

FT tag= a

FT tag= a

FT tag= a

FT tag= a

FT tag= a

FT tag= a

FT tag= a

priority

Itoh N, Nagata S, Yonehara S;

WPI; 1992-358914/44.

P-PSDB; AAR28084.

DNA encoding human cell surface antigen - used to clarify

apoptosis mechanism of various types of cell, and to prepare

monoclonal antibodies that react with tumour cells expressing Fas

FT sig_peptide 195..242
FT /*tag= b
FT mat_peptide 243..1199
FT /*tag= c

PN JP07115988-A.

XX 09-MAY-1995.

XX 26-OCT-1993; 93JP-0267644.

XX 26-OCT-1993; 93JP-0267644.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 1995-202847/27.

XX P-PSDB; AAR78606.

XX Preparation of soluble membrane proteins - for their use in antibody
PT production for the treatment and prevention of related diseases

XX Example 1; Pages 15-17; 51pp; Japanese.

XX AAQ5297 is the plasmid pF58 which contains the human Fas cDNA. The
CC plasmid was used in the construction of an expression vector for
CC the prodn. of recombinant soluble membrane proteins. The proteins
CC can be used in antibody prodn. for the treatment and prevention of
CC related diseases.

XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 16; Length 2534;
Best Local Similarity 100.0%; Pred. No. 2.6e-108;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAGGAGTACAGAAACATCGAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 60
DB 765 AAGAGAAAGGAGTACAGAAACATCGAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 824

OY 61 GAATCTCCACCTTAAATCCTGAACAGTGGCAATATTTATCTGATGTGACTTGAGT 120
DB 825 GAATCTCCACCTTAAATCCTGAACAGTGGCAATATTTATCTGATGTGACTTGAGT 884

OY 121 AAATATATCACCACCTATTTGCTGGAGTCAATAGTCAAGTAAAGGCTTTGTTTGA 180
DB 885 AAATATATCACCACCTATTTGCTGGAGTCAATAGTCAAGTAAAGGCTTTGTTTGA 944

OY 181 AAGAATGGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGTCTCAAGACACA 240
DB 945 AAGAATGGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGTCTCAAGACACA 1004

OY 241 GCAGAACAGAAAGTTCACTGCTTGGTAAATGGCAATCACTTCAAGAAAGAAAGCG 300
DB 1005 GCAGAACAGAAAGTTCACTGCTTGGTAAATGGCAATCACTTCAAGAAAGAAAGCG 1064

OY 301 TATGACACATGATTAAAGATCTCAAAAGGCCAATCTTGTACTCTTGCAGAGAAAT 360
DB 1065 TATGACACATGATTAAAGATCTCAAAAGGCCAATCTTGTACTCTTGCAGAGAAAT 1124

OY 361 CAGACTATATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTTCAAACTTCAAGAAATGAA 420
DB 1125 CAGACTATATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTTCAAACTTCAAGAAATGAA 1184

OY 421 ATCCAAAGCTGGTC 435

DB 1185 ATCCAAAGCTGGTC 1199

RESULT 11

AAT16303

ID AAT16303 standard; cDNA; 2534 BP.

XX

AC AAT16303;

XX

DT

XX

DE

XX

KW

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KW

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06-SEP-1996 (first entry)

hFas coding sequence from plasmid pCEV4/hFas.

Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
rheumatoid arthritis; serum; systemic lupus erythematosus; ss.

Synthetic.

Location/Qualifiers

195..1201

/tag= a

/product= Fas antigen

195..242

/tag= b

243..1998

/tag= c

WO9601277-A1.

18-JAN-1996.

03-MAR-1995; 95WO-JP00349.

14-FEB-1995; 95JP-0025637.

06-JUL-1994; 94JP-0154706.

(MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.

(NISB) JAPAN TOBACCO INC.

Hachiya T, Noguchi J, Yonehara S;

WPI; 1996-087635/09.

P-PSDB; AAR92528.

Immunosay method for soluble Fas antigen in body fluids - for

diagnosis of autoimmune diseases such as rheumatoid arthritis and

systemic lupus erythematosus

Example 8; Page 49-52; 124pp; Japanese.

This sequence represents the coding sequence for the human Fas antigen

contained within the plasmid pCEV4/hFas. The soluble Fas antigen is

included in the immunoassay kit of the invention. The kit is for the

assay of soluble Fas antigen and contains an immobilised anti-soluble Fas

monoclonal antibody, as well as the standard soluble Fas antigen encoded

by this sequence. The assay is simple and has high accuracy, high

sensitivity, and is capable of assaying a number of different specimens

at the same time. The immunoassay is used on biological samples (such as

serum) and is useful for diagnosis of autoimmune diseases such as

rheumatoid arthritis or systemic lupus erythematosus (SLE).

Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 17; Length 2534;

Best Local Similarity 100.0%; Pred. No. 2.6e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAGGAGTACAGAAACATCGAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 60

DB 765 AAGAGAAAGGAGTACAGAAACATCGAGAAAGCAGAGAAAGGAAACCAAGTTCTCAT 824

OY 61 GAATCTCCACCTTAAATCCTGAACAGTGGCAATATTTATCTGATGTGACTTGAGT 120

DB 825 GAATCTCCACCTTAAATCCTGAACAGTGGCAATATTTATCTGATGTGACTTGAGT 884

OY 121 AAATATATCACCACCTATTTGCTGGAGTCAATAGTCAAGTAAAGGCTTTGTTTGA 180

DB 885 AAATATATCACCACCTATTTGCTGGAGTCAATAGTCAAGTAAAGGCTTTGTTTGA 944

OY 181 AAGAATGGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGTCTCAAGACACA 240

DB 945 AAGAATGGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGTCTCAAGACACA 1064

OY 241 GCAGAACAGAAAGTTCACTGCTTGGTAAATGGCAATCACTTCAAGAAAGAAAGCG 300

DB 1005 GCAGAACAGAAAGTTCACTGCTTGGTAAATGGCAATCACTTCAAGAAAGAAAGCG 1064

OY 301 TATGACACATGATTAAAGATCTCAAAAGGCCAATCTTGTACTCTTGCAGAGAAAT 360

DB 1065 TATGACACATGATTAAAGATCTCAAAAGGCCAATCTTGTACTCTTGCAGAGAAAT 1124

OY 361 CAGACTATATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTTCAAACTTCAAGAAATGAA 420

DB 1125 CAGACTATATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTTCAAACTTCAAGAAATGAA 1184

OY 421 ATCCAAAGCTGGTC 435

DB 1185 ATCCAAAGCTGGTC 1199

Db 945 AAGATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAATGTCCAAGACACA 1004
 Qy 241 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCACTCAATGGAAGAAAGAGCG 300
 Db 1005 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCACTCAATGGAAGAAAGAGCG 1064
 Qy 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAATTT 360
 Db 1065 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAATTT 1124
 Qy 361 CAGACTATCATCCCTCAAGGACATTTACTAGTGACTCAGAAAAATTTCAAACTTCAGAAATGAA 420
 Db 1125 CAGACTATCATCCCTCAAGGACATTTACTAGTGACTCAGAAAAATTTCAAACTTCAGAAATGAA 1184
 Qy 421 ATCCAAAGCTTGGTC 435
 Db 1185 ATCCAAAGCTTGGTC 1199

RESULT 12

AAV07002 ID AAV07002 standard; cDNA to mRNA; 2534 BP.

XX AC AAV07002;
 XX DF 16-JUL-1998 (first entry)
 XX DE Human Fas antigen cDNA.

XX KW Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
 KW apoptosis modulation; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX CDS 195..1202
 FT /*tag= a
 FT sig_peptide 195..242
 FT /*tag= b
 FT mat_peptide 243..1199
 FT /*tag= c
 FT /*product= Fas_antigen

XX PN M09742319-A1.

XX PD 13-NOV-1997.

XX PF 01-MAY-1997; 97MO-JP01502.

XX PR 02-MAY-1996; 96JP-0135760.

XX PA (MOCH) MOCHIDA PHARM CO LTD.
 XX PA (OSAB-) OSAKA BIOSCIENCE INST.

XX PI Negata S, Nakamura N;

XX XX WPI; 1997-558981/51.

XX P-PSDB; AAW50289.

XX PT Fas antigen derivative containing modified extracellular region -
 PT has low antigenicity, promotes apoptosis and is useful in treatment
 PT of viral and other diseases

XX PS Disclosure; Fig 1-2; 102pp; Japanese.

XX CC The present sequence was used in the development of novel Fas
 CC antigen derivatives, which contain a Fas antigen extracellular
 CC region lacking one or more amino acid residues in the region from
 CC the amino-terminal to (but excluding) the 1st cysteine residue
 CC (preferably at least 29 residues are deleted).
 CC The derivatives are effective regulators of apoptosis and can be
 CC used (either by administration of the polypeptide, or by the use

CC of the coding DNA in gene therapy) to treat a range of diseases,
 CC e.g. diabetes, arthritis, lupus and in particular viral diseases
 CC such as hepatitis, influenza and HIV; by modulating apoptosis of
 CC virus-infected cells.

XX SQ Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 18; Length 2534;
 Best Local Similarity 100.0%; Pred. No. 2.6e-108;
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAAAACCAAGGTTCTCAT 60
 Db 765 AAGAGAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAAAACCAAGGTTCTCAT 824
 Qy 61 GAATCTCCAACCTTAAATCTCTGAACAGAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
 Db 825 GAATCTCCAACCTTAAATCTCTGAACAGAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 884
 Qy 121 AATATATATCACTACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTTTCA 180
 Db 885 AATATATATCACTACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTTTCA 944
 Qy 181 AAGATGCTGTCAATGAAGCAGAAATAGATGAGATCAAGATGACAATGTCCAAGACACA 240
 Db 945 AAGATGCTGTCAATGAAGCAGAAATAGATGAGATGACAATGTCCAAGACACA 1004
 Qy 241 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCACTTCAATGGAAGAAAGAGCG 300
 Db 1005 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCACTTCAATGGAAGAAAGAGCG 1064
 Qy 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAATTT 360
 Db 1065 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAATTT 1124
 Qy 361 CAGACTATCATCCCTCAAGGACATTTACTAGTGACTCAGAAAAATTTCAAACTTCAGAAATGAA 420
 Db 1125 CAGACTATCATCCCTCAAGGACATTTACTAGTGACTCAGAAAAATTTCAAACTTCAGAAATGAA 1184
 Qy 421 ATCCAAAGCTTGGTC 435
 Db 1185 ATCCAAAGCTTGGTC 1199

RESULT 13

AAV32993

ID AAV32993 standard; cDNA; 2534 BP.

XX AC AAV32993;

XX DF 18-NOV-1998 (first entry)

XX DE Fas cDNA.

XX KW Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
 KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
 KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
 KW prophylactic; AIDS; ss.

XX OS Mammalia sp.

XX FH Key Location/Qualifiers

XX CDS 195..1202
 FT /*tag= a
 FT /*product= "Fas protein"
 FT sig_peptide 195..242
 FT /*tag= b
 FT mat_peptide 243..1199
 FT /*tag= c
 FT polyA_signal 1831..1836
 FT /*tag= d

XX PN M09835692-A1.

XX PD 20-AUG-1998.
XX PF 17-FEB-1998; 98WO-GB00485.
XX PR 17-FEB-1997; 97GB-0003276.
XX PA (ISIS-) ISIS INNOVATION LTD.
XX PI Sreaton GR, Xu X;
XX WP1: 1998-456867/39.
DR P-PSDB; AAW49104.
XX
PT Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
PT diseases - by interfering with interaction of Fas with Fas-ligand
PT expressed on activated CD4+ cells, e.g. cells infected with HIV
XX
PS Disclosure; Fig 10; 71pp; English.
XX
CC The present sequence represents a Fas cDNA sequence used in the
CC method of the invention. The method is concerned with reducing
CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
CC cells in an immune cell population which also comprises of Fas-ligand
CC (FasL)-expressing activated CD4+ cells. It involves contacting this
CC immune cell population with an effective amount of an agent (e.g. a
CC soluble Fas-Fc fusion protein) which would interfere with the
CC interaction between Fas and FasL. Therefore, the method is useful for
CC identifying suitable agents which can reduce depletion of activated
CC Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
CC is the use of the agent in the manufacture of therapeutic compositions.
CC Apoptosis of lymphocytes can be triggered by the interaction of the
CC cell surface receptor Fas and its ligand FasL. By interfering with
CC this interaction, the method described and its preparations can prevent
CC apoptosis of CD8+ TK lymphocytes caused by expression of FasL on
CC activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
CC especially the result of CD4+ cell infection with an immunodeficiency
CC virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
CC virus (SIV). The claimed prevention of apoptosis may then allow
CC maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
CC towards the CD4+ cells infected with the infectious agent, enabling
CC treatment (prophylactic and/or therapeutic) of immunodeficiency
CC diseases e.g. AIDS.
XX
SQ Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 19; Length 2534;
Best Local Similarity 100.0%; Pred. No. 2.6e-108;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 60
DB 765 AGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 824
OY 61 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
DB 825 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 884
OY 121 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTCGA 180
DB 885 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTCGA 944
OY 181 AGAATGGTGTCAATCAAGCCAAATAGATGATGATCAAGATCAAGATGATCAAGACACA 240
DB 945 AGAATGGTGTCAATCAAGCCAAATAGATGATGATCAAGATGATCAAGATGATCAAGACACA 1004
OY 241 GCAGAACAGAAAGTCTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGGCG 300
DB 1005 GCAGAACAGAAAGTCTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGGCG 1064
OY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAAT 360
DB 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAAT 1124

OY 361 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTCAGAAATTCAGAAATGAA 420
DB 1125 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTCAGAAATTCAGAAATGAA 1184
OY 421 ATCCAAAGCTTGGTC 435
DB 1185 ATCCAAAGCTTGGTC 1199
RESULT 14
AAC61798
ID AAC61798 standard; DNA; 2551 BP.
XX
AC AAC61798;
XX
DT 06-MAR-2001 (first entry)
XX
DE DNA encoding a human Fas (Apo-1) protein.
XX
KW Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;
KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
KW autoimmune disease; inflammatory disease; lymphoma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 221..1228
FT /tag= a
FT /product= "Fas"
XX
PN WO200061150-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US09540.
XX
PR 12-APR-1999; 99US-0290640.
XX
PA (ISIS-) ISIS PHARM INC.
PI Dean NM, Marcussen EG;
XX
XX WP1: 2000-628395/60.
DR P-PSDB; AAB19341.
XX
PT Antisense oligonucleotides for treating hepatitis and colon, liver or
PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
PT 1 (Fas-1) expression
XX
PS Example 2; Page 71-73; 116pp; English.
XX
CC The present sequence encodes human Fas (Apo-1). The specification
CC describes antisense compounds which are targeted to the 5'-untranslated
CC region, translational start site, translational termination region
CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
CC ligand (FasL), or Fas-1 (Fas associated protein 1, protein tyrosine
CC phosphatase). The antisense compounds are used to inhibit the
CC expression of Fas, FasL or Fas-1 in cells or tissues. They are used
CC to treat autoimmune or inflammatory diseases such as hepatitis. They
CC can also be used to treat cancer, especially colon, liver or lung
CC cancer or lymphoma.
XX
SQ Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;

Query Match 100.0%; Score 435; DB 21; Length 2551;
Best Local Similarity 100.0%; Pred. No. 2.6e-108;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 60
DB 791 AGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 850

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:17:33 ; Search time 65 Seconds
(without alignments)
2052.375 Million cell updates/sec

Title: US-09-884-987-1_COPY_765_1199
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Sequence: 1 aagagaaggaagtagacagaa.....atgaatccaagcttggtc 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	857	5	PCT-US95-17083-9
2	435	100.0	920	5	PCT-US95-17083-7
3	435	100.0	1104	5	PCT-US95-17083-3
4	435	100.0	1167	5	PCT-US95-17083-1
5	435	100.0	2471	1	US-08-444-231-18
6	435	100.0	2471	1	US-08-152-443A-18
7	435	100.0	2534	2	US-08-219-237B-1
8	435	100.0	2534	4	US-08-468-560C-1
9	435	100.0	2534	4	US-09-180-100-16
10	435	100.0	2551	4	US-09-290-640-1
11	354	81.4	975	5	PCT-US95-17083-5
12	167.6	38.5	1480	4	US-09-290-640-65
13	50.4	11.6	7218	1	US-08-232-463-14
14	43	9.9	1956	4	US-08-559-898B-1
15	39	9.0	2706	2	US-08-630-822A-61
16	39	9.0	2706	2	US-09-005-069-61
17	39	9.0	2706	4	US-09-171-156A-20
18	38.2	8.8	2268	1	US-08-444-005-14
19	36.8	8.5	9244	4	US-08-961-527-68
20	36.6	8.4	2277	1	US-08-676-967-2
21	36.6	8.4	2277	1	US-08-676-974-2
22	36.6	8.4	2277	2	US-09-098-487-2
23	36	8.3	1000	4	US-09-222-938A-35
24	34.4	7.9	1054	1	US-08-393-985-7
25	33.2	7.6	903	4	US-09-134-001C-1548
26	33.2	7.6	1398	4	US-09-134-001C-1019
27	32.8	7.5	957	1	US-08-349-696-26

c 28	32.8	7.5	957	1	US-08-233-009-26	Sequence 26, Appl
c 29	32.8	7.5	957	1	US-08-560-231-26	Sequence 26, Appl
c 30	32.8	7.5	957	4	US-09-080-704A-26	Sequence 26, Appl
c 31	32.8	7.5	1789	2	US-08-895-521-2	Sequence 2, Appl
c 32	32.8	7.5	1789	3	US-09-235-218-2	Sequence 2, Appl
c 33	32.8	7.5	1962	3	US-08-714-918-18	Sequence 18, Appl
c 34	32.8	7.5	1962	4	US-09-265-315-18	Sequence 18, Appl
c 35	32.8	7.5	1962	4	US-09-265-315-18	Sequence 18, Appl
c 36	32.8	7.5	1962	4	US-09-266-417-18	Sequence 18, Appl
c 37	32.6	7.5	1056	4	US-09-134-001C-2655	Sequence 2655, Ap
c 38	32.4	7.4	760	2	US-08-474-379C-78	Sequence 78, Appl
c 39	32.4	7.4	760	3	US-09-146-249A-78	Sequence 78, Appl
c 40	32.4	7.4	760	3	US-08-206-188B-78	Sequence 78, Appl
c 41	32.4	7.4	1649	2	US-07-688-352C-35	Sequence 35, Appl
c 42	32.4	7.4	1649	2	US-08-474-379C-35	Sequence 35, Appl
c 43	32.4	7.4	1649	3	US-09-146-249A-35	Sequence 35, Appl
c 44	32.4	7.4	1649	3	US-08-206-188B-35	Sequence 35, Appl
c 45	32.4	7.4	1649	5	PCT-US91-02714-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
PCT-US95-17083-9
; Sequence 9, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 857 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-9

Query Match	100.0%	Score 435;	DB 5;	Length 857;
Best Local Similarity	100.0%	Pred. No. 3.1e-109;		
Matches 435;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGAGAAAGCAAGGTTCTCAT	60	
DB	286	AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGAGAAAGCAAGGTTCTCAT	345	
QY	61	GAATCTCAACCTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACCTGAGT	120	
DB	346	GAATCTCAACCTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACCTGAGT	405	
QY	121	AAATATATCACCACATTTGCTGAGTCATGACACATGAAGTAAAGGCTTTGTTCCA	180	
DB	406	AAATATATCACCACATTTGCTGAGTCATGACACATGAAGTAAAGGCTTTGTTCCA	465	
QY	181	AAGAATGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA	240	
DB	466	AAGAATGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA	525	
QY	241	GCAGAACAGAAAGTCAACTGCTTCGTAATGGCATCAACTTCATGGGAAGAAAGACGG	300	
DB	526	GCAGAACAGAAAGTCAACTGCTTCGTAATGGCATCAACTTCATGGGAAGAAAGACGG	585	
QY	301	TATGACACATTTAAAGATCTCAAAAAGCAATCTTTGTACTCTTGCAGAGAAATTT	360	
DB	586	TATGACACATTTAAAGATCTCAAAAAGCAATCTTTGTACTCTTGCAGAGAAATTT	645	

QY 361 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAAATTCAGAAATGAA 420
Db 646 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAAATTCAGAAATGAA 705
QY 421 ATCCAAAGCTTGGTC 435
Db 706 ATCCAAAGCTTGGTC 720

RESULT 2

PCT-US95-17083-7

; Sequence 7, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: CONCURRENTLY HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 920 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US95-17083-7

Query Match 100.0%; Score 435; DB 5; Length 920;

Best Local Similarity 100.0%; Pred. No. 3.2e-109;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAAGTACAGAAAACATGCGAGAAAGCAGACAGAAAGGAAAGGAAAGGTTCTCAT 60
Db 349 AAGAGAAAGGAAAGTACAGAAAACATGCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 408
QY 61 GAATCTCAACCTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120
Db 409 GAATCTCAACCTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 468
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 180
Db 469 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 528
QY 181 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 240
Db 529 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 588
QY 241 GCAGAACAGAAAGTCAACTGCTTCGTAATGGGCACTCACTTTCATGGAAGAAAGAGCG 300
Db 589 GCAGAACAGAAAGTCAACTGCTTCGTAATGGGCACTCACTTTCATGGAAGAAAGAGCG 648
QY 301 TATGACATATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 360
Db 649 TATGACATATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 708
QY 361 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAAATTCAGAAATGAA 420
Db 709 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAAATTCAGAAATGAA 768
QY 421 ATCCAAAGCTTGGTC 435
Db 769 ATCCAAAGCTTGGTC 783

RESULT 3

PCT-US95-17083-3

; Sequence 3, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: CONCURRENTLY HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1167 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-3

Query Match

100.0%; Score 435; DB 5; Length 1104;

Best Local Similarity 100.0%; Pred. No. 3.4e-109;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAAGTACAGAAAACATGCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 60
Db 533 AAGAGAAAGGAAAGTACAGAAAACATGCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 592
QY 61 GAATCTCAACCTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120
Db 593 GAATCTCAACCTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 652
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 180
Db 653 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 712
QY 181 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 240
Db 713 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 772
QY 241 GCAGAACAGAAAGTCAACTGCTTCGTAATGGGCACTCACTTTCATGGAAGAAAGAGCG 300
Db 773 GCAGAACAGAAAGTCAACTGCTTCGTAATGGGCACTCACTTTCATGGAAGAAAGAGCG 832
QY 301 TATGACATATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 360
Db 833 TATGACATATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 892
QY 361 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAAATTCAGAAATGAA 420
Db 893 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAAATTCAGAAATGAA 952
QY 421 ATCCAAAGCTTGGTC 435
Db 953 ATCCAAAGCTTGGTC 967

RESULT 4

PCT-US95-17083-1

; Sequence 1, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: CONCURRENTLY HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1167 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

TOPOLOGY: linear
PCT-US95-17083-1

Query Match 100.0%; Score 435; DB 5; Length 1167;
Best Local Similarity 100.0%; Pred. No. 3.4e-109;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGGAAAGGTTCTCAT 60
DB 596 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGGAAAGGTTCTCAT 655
QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
DB 656 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 715
QY 121 AAATATATCACCACATTTGCTGGAGTCATGACACTAACTGCAAGTTAAAGGGCTTTGTTTGA 180
DB 716 AAATATATCACCACATTTGCTGGAGTCATGACACTAACTGCAAGTTAAAGGGCTTTGTTTGA 775
QY 181 AAGATGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 240
DB 776 AAGATGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 835
QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGACGC 300
DB 836 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGACGC 895
QY 301 TATGACACATTTGATTAAAGATCTCAAAAAGCCAACTTTTGTACTCTTTCGAGAGAAAATT 360
DB 896 TATGACACATTTGATTAAAGATCTCAAAAAGCCAACTTTTGTACTCTTTCGAGAGAAAATT 955
QY 361 CAGACTATCATCTCCCAAGGACATTAAGTACTAGTCAAGAAATTCAGAAATTCAGAAATGAA 420
DB 956 CAGACTATCATCTCCCAAGGACATTAAGTACTAGTCAAGAAATTCAGAAATTCAGAAATGAA 1015
QY 421 ATCCAAAGCTTGGTC 435
DB 1016 ATCCAAAGCTTGGTC 1030

RESULT 5

US-08-444-231-18
; Sequence 18, Application US/08444231
; Patent No. 5652210

GENERAL INFORMATION:

; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0 Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444/231
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/452,443
; FILING DATE: 15-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943

; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2471 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 195..1136

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 243

US-08-444-231-18

Query Match 100.0%; Score 435; DB 1; Length 2471;

Best Local Similarity 100.0%; Pred. No. 4.4e-109;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGGAAAGGTTCTCAT 60
DB 702 AAGAGAAAGGAGTACAGAAACATGCGAAGACGACAGAAAGGAAAGGTTCTCAT 761
QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
DB 762 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 821
QY 121 AAATATATCACCACATTTGCTGGAGTCATGACACTAACTGCAAGTTAAAGGGCTTTGTTTGA 180
DB 822 AAATATATCACCACATTTGCTGGAGTCATGACACTAACTGCAAGTTAAAGGGCTTTGTTTGA 881
QY 181 AAGATGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 240
DB 882 AAGATGTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 941
QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGACGC 300
DB 942 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGACGC 1001
QY 301 TATGACACATTTGATTAAAGATCTCAAAAAGCCAACTTTTGTACTCTTTCGAGAGAAAATT 360
DB 1002 TATGACACATTTGATTAAAGATCTCAAAAAGCCAACTTTTGTACTCTTTCGAGAGAAAATT 1061
QY 361 CAGACTATCATCTCCCAAGGACATTAAGTACTAGTCAAGAAATTCAGAAATTCAGAAATGAA 420
DB 1062 CAGACTATCATCTCCCAAGGACATTAAGTACTAGTCAAGAAATTCAGAAATTCAGAAATGAA 1121
QY 421 ATCCAAAGCTTGGTC 435
DB 1122 ATCCAAAGCTTGGTC 1136

RESULT 6

US-08-152-443A-18
; Sequence 18, Application US/08152443A
; Patent No. 5663070

GENERAL INFORMATION:

; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-2006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-152-443A-18

Query Match 100.0%; Score 435; DB 1; Length 2471;
Best Local Similarity 100.0%; Pred. No. 4.4e-109;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT	60
Db	702	AAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT	761
Qy	61	GAATCTCAACCTTAATCTGGAAGTGCAGCAATTAATCTGATGTTGACTTCAGT	120
Db	762	GAATCTCAACCTTAATCTGGAAGTGCAGCAATTAATCTGATGTTGACTTCAGT	821
Qy	121	AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA	180
Db	822	AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA	881
Qy	181	AAGAATGGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCACAGACACA	240
Db	882	AAGAATGGTCAATGAAGCAAAATAGATGAGATGACAAATGTCACAGACACA	941
Qy	241	GCAGAACAGAAAGTCAACTGCTTCGTAATGGCATCAACTTCATGGAAGAAAGAGCG	300
Db	942	GCAGAACAGAAAGTCAACTGCTTCGTAATGGCATCAACTTCATGGAAGAAAGAGCG	1001
Qy	301	TATGACACATTTGATTAAGATCTCAAAAAGCAATCTTTGTTACTCTTTCAGAGAAAT	360
Db	1002	TATGACACATTTGATTAAGATCTCAAAAAGCAATCTTTGTTACTCTTTCAGAGAAAT	1061
Qy	361	CAGACTATATCTCTCAAGGACATTAAGTACTGAGTCAAGAAATTCAAATTCAGAAATGAA	420
Db	1062	CAGACTATATCTCTCAAGGACATTAAGTACTGAGTCAAGAAATTCAAATTCAGAAATGAA	1121
Qy	421	ATCCAAGCTTGGTC	435
Db	1122	ATCCAAGCTTGGTC	1136

RESULT 7

US-08-219-237B-1
; Sequence 1, Application US/08219237B
; Patent No. 5674546

GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: pCEV4
CLONE: clone pf58
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2518..2523
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
US-08-219-237B-1


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SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1202
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 195..242
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243..1199
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1831..1836
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2352..2357
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2518..2532
US-08-468-560C-1

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Query Match	100.0%;	Score 435;	DB 4;	Length 2534;
Best Local Similarity	100.0%;	Pred. No. 4.5e-109;		
Matches 435;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AAAGAGAAGCAACTACAGAAAACATGCAGAAAGCAGACAGAAAGCAAAACCAAGCTTCTCAT	60	
Db	765	AAAGAGAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGCAAAACCAAGGTTCTCAT	824	
Qy	61	GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTTGAGT	120	
Db	825	GAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT	884	
Qy	121	AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCTGA	180	
Db	885	AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCTGA	944	
Qy	181	AGAAATGGTGTCAAATGAAGCCAAATATAGATGAGATCAAGAATGACAAATGTCCAAGACACA	240	
Db	945	AGAATGGTGTCAAATGAAGCCAAATATAGATGAGATCAAGAATGACAAATGTCCAAGACACA	1004	
Qy	241	GCAGACAGAAAGCTTCAACTGCTTCGTAATTTGGCATCAACTTCATGAAAGAAGAAGCG	300	
Db	1005	GCAGACAGAAAGCTTCAACTGCTTCGTAATTTGGCATCAACTTCATGAAAGAAGAAGCG	1064	
Qy	301	TATGACACATTGATTTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTCGACAGAGAAAATT	360	
Db	1065	TATGACACATTGATTTAAAGATCTCAAAAAGCCAATCTTTGTACTCTTCGACAGAGAAAATT	1124	
Qy	361	CAGACTATCATCTCTCAAGGCATTACTAGTGACTCAGAAAAATTCAAACTTTCAGAAATGAA	420	
Db	1125	CAGACTATCATCTCTCAAGGCATTACTAGTGACTCAGAAAAATTCAAACTTTCAGAAATGAA	1184	
Qy	421	ATCCAAAGCTTGGTC	435	
Db	1185	ATCCAAAGCTTGGTC	1199	

RESULT 9
US-09-180-100-16
; Sequence 16, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: MUGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180.100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-03-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 2534
TYPE: DNA
ORGANISM: Homo sapiens
US-09-180-100-16

Query Match 100.0%; Score 435; DB 4; Length 2534;
Best Local Similarity 100.0%; Pred. No. 4.5e-109;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 60
Db 765 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 824
Qy 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
Db 825 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 884
Qy 121 AATATATACACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180
Db 885 AATATATACACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 944
Qy 181 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 240
Db 945 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 1004
Qy 241 GCAGACAGAAAGTTCAACTGCTTGAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300
Db 1005 GCAGACAGAAAGTTCAACTGCTTGAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 1064
Qy 301 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAT 360
Db 1065 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAT 1124
Qy 361 CAGACTATCATCTCCAGGACATTACTAGTGACTCAGAAAAATTCAGAAATGAA 420
Db 1125 CAGACTATCATCTCCAGGACATTACTAGTGACTCAGAAAAATTCAGAAATGAA 1184
Qy 421 ATCCAAAGCTTGGTC 435
Db 1185 ATCCAAAGCTTGGTC 1199

RESULT 10
US-09-290-640-1
Sequence 1, Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290.640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267

ISSUE: 15
PAGES: 10709-10715
DATE: 1992-05-25
DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1

Query Match 100.0%; Score 435; DB 4; Length 2551;
Best Local Similarity 100.0%; Pred. No. 4.5e-109;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 60
Db 791 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 850
Qy 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
Db 851 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 910
Qy 121 AATATATACACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180
Db 911 AATATATACACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 970
Qy 181 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 240
Db 971 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 1030
Qy 241 GCAGACAGAAAGTTCAACTGCTTGAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300
Db 1031 GCAGACAGAAAGTTCAACTGCTTGAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 1090
Qy 301 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAT 360
Db 1091 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAT 1150
Qy 361 CAGACTATCATCTCCAGGACATTACTAGTGACTCAGAAAAATTCAGAAATGAA 420
Db 1151 CAGACTATCATCTCCAGGACATTACTAGTGACTCAGAAAAATTCAGAAATGAA 1210
Qy 421 ATCCAAAGCTTGGTC 435
Db 1211 ATCCAAAGCTTGGTC 1225

RESULT 11
PCT-US95-17083-5
Sequence 5, Application PC/TUS9517083
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-17083-5

Query Match 81.4%; Score 354; DB 5; Length 975;
Best Local Similarity 100.0%; Pred. No. 3.1e-87;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATACACACTATTGCT 141
Db 485 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATACACACTATTGCT 544

Query Match	38.5%	Score 167.6	DB 4	Length 1480		
Best Local Similarity	63.3%	Pred. No. 1.4e-36				
Matches 257	Conservative	0	Mismatches 149	Indels 0	Gaps 0	
QY	28	AGAAAGCCACAGAAAGGAAACCAAGGTTCTCATGAATCTCCAACCTTAATCTCTGAACA	87			
DB	623	AGAAAGTCTGGAAAGGAGACAGATGACCCCTGAATCTAGAACCCTCAGCTCGTGAAC	582			
QY	88	GTGGCAATAAATTTATCTGATGTTTGACTTGAGTAAATATATACCCACTATTGCTGGAGTC	147			
DB	683	ATACCAATGAATGCCTCAAATCTTAGCTTGAGTAAATACATCCGAGAAATGCTGAAGAC	742			
QY	148	ATGACACTTAAGTCAAGTTAAAGGCTTTGTTCGAAGAAGTGGTGTCAATGAAGCCAAANTA	207			
DB	743	ATGACATCCAGGAAGCTTAAAAAATTTTCTCGAAAAAATAACATCAAGAGGGGCAAGATA	802			
QY	208	GATGAGATCAAGAATGACAATGTCCAAGACACAGACAAGAAAGTTCAACTGCTTCGT	267			
DB	803	GATGAGATCATGTCATGACACGATCCAGACACACTGAGCAGAAAGTCCAGCTTGCTCCTG	862			
QY	268	AATTGGCATCAACTTTCATGGAAAGAAAGACGCTATGACACATTTGATTAAAGATCTCAA	327			

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Db      863  TGCTGTGTAACCAATCTCATGGAAGAGATGATGCATATATCAAGATTTAATCAAGGCTCTCAA 922
Qy      328  AAAGCCCAATCTTTGTACTCTTGCAGAGAAAATTCAGACATATATCTCTCAAGGACATTACT 387
Db      923  AAAGCCCAATGTGCGAGAACCTTTAGATAAATTTTCAGGACATGCTCCAGAAGGACCTTGG 982
Qy      388  AGTGACTTCAGAAAATTCAAACTTCAGAAATGAATGAATCAAAAGCTTGG 433
Db      983  AAATCAACCCAGACACATGGAATGAATAATGAAGGACAATGTCTGG 1028

RESULT 13.
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFELINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 11.6%; Score 50.4; DB 1; Length 7218;
Best Local Similarity 4.2%; Pred. No. 0.00015;
Matches 15; Conservative 200; Mismatches 141; Indels 0; Gaps 0;

Qy      1  AAGAGAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAAACCAAGTTCTCAT 60
Db      1394  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1395
Qy      61  GAATCTCAACCTTAATCTCTGAACAGTGGCAATAAATTATCTGATGTTGACTTCAGT 120
Db      1334  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1275
Qy      121  AAATATATACCACTATTGCTGGAGTCATGACACATAAGTCAAGTTAAAGGCTTGTTCGA 180

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QY	244	GAACAGAAAGTTCAACTGCTTCGTAATGGCATCAACTTCATGGAAGAAAGAGCGTAT	303
Db	2414	GAACCTTAGGAGAACTTGAGGAAATCTCGTCATATTCAAGAAATGGAGAGAAAGA	2473
QY	304	GACACATTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAAATTCAG	363
Db	2474	GAAAGTTTGGTTCATCAGCTACAAATTCGATTAGCTAGAGCTGATTCAGAGGCATTGGCG	2533
QY	364	ACTATCATCTCAAGGACATTTACTAGTGAATCAGAAAATTCAGAAATGAAATC	423
Db	2534	AGATCAATAGCTGATGAAAGTATAGCTGATTTAGAAAAGGAAAGACTATGAAGGAATTA	2593
QY	424	CAA	426
Db	2594	GAA	2596

Search completed: June 15, 2003, 21:13:05
Job time : 66 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:47:53 ; Search time 126 Seconds
(without alignments)
4999.257 Million cell updates/sec

Title: US-09-884-987-1_COPY_765_1199

Perfect score: 435
Sequence: 1 aagagaaggagtagtacagaa.....atgaataccaagcttgctc 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0:
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications, NA:*
- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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 - 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 - 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 - 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
 - 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	836	10	US-09-802-669-102
2	435	100.0	2534	10	US-09-949-713-16
3	435	100.0	2534	10	US-09-884-987-1
4	435	100.0	2551	10	US-09-802-669-1
5	435	100.0	8282	9	US-09-966-976A-7
6	435	100.0	8282	9	US-09-963-206B-7
7	435	100.0	8345	9	US-09-966-976A-8
8	435	100.0	8345	9	US-09-966-976A-8
9	404.2	92.9	490	9	US-09-918-995-17119
10	394.4	90.7	398	10	US-09-867-701-2490
11	383.6	88.2	468	10	US-09-867-701-3156
12	354	81.4	975	9	US-09-954-531-998
13	330	75.9	1840	10	US-09-802-669-101
14	302	69.4	489	9	US-09-918-995-13045
15	302	69.4	496	9	US-09-918-995-15171
16	224.8	51.7	447	9	US-09-918-995-7395
17	167.6	38.5	1480	10	US-09-802-669-65
18	83.4	19.2	338	10	US-09-802-669-99
19	43	9.9	1956	10	US-09-351-794A-1

ALIGNMENTS

RESULT 1

US-09-802-669-102

; Sequence 102, Application US/09802669

; Patent No. US20020004490A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Marcussen, Eric G.

; APPLICANT: Wyatt, Jacqueline

; APPLICANT: Zhang, Hong

; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

; FILE REFERENCE: ISPH-545

; CURRENT APPLICATION NUMBER: US/09-802,669

; CURRENT FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: US/09/665,615

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: US/09/290,640

; PRIOR FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 102

; LENGTH: 836

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(399)

US-09-802-669-102

Query Match 100.0%; Score 435; DB 10; Length 836;

Best Local Similarity 100.0%; Pred. No. 8e-104;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAGAGAAAGGAGTAGTACAGAAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT	60
Db	399	AGAGAAAGGAGTAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT	458
QY	61	GAATCTCCAACTTAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT	120
Db	459	GAATCTCCAACTTAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT	518
QY	121	AAATATATACCACTATTCTGAGTTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGA	180

Db 519 AAATATATACACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTCGA 578
QY 181 AAGATGCTGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATCTCCAAGACACA 240
Db 579 AAGATGCTGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATCTCCAAGACACA 638
QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 300
Db 639 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 698
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 360
Db 699 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 758
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAAATTTCAAACTTCAGAAATGAA 420
Db 759 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAAATTTCAAACTTCAGAAATGAA 818
QY 421 ATCCAAAGCTTGGTC 435
Db 819 ATCCAAAGCTTGGTC 833

RESULT 2

US-09-949-713-16
; Sequence 16, Application US/09949713
; Patent No. US20020044944A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. US20020044944A1
; APPLICANT: NAKAMURA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-713-16

Query Match 100.0%; Score 435; DB 10; Length 2534;
Best Local Similarity 100.0%; Pred. No. 1.4e-103;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 60
Db 765 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 824
QY 61 GAATCTCAACCTTAAATCTTGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120
Db 825 GAATCTCAACCTTAAATCTTGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 884
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 180
Db 885 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 944
QY 181 AAGATGCTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 240
Db 945 AAGATGCTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 1004
QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 300
Db 1005 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 1064
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 360
Db 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 1124
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAAATTTCAAACTTCAGAAATGAA 420
Db 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 1124

QY 361 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAAATTTCAAACTTCAGAAATGAA 420
Db 1125 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAAATTTCAAACTTCAGAAATGAA 1184
QY 421 ATCCAAAGCTTGGTC 435
Db 1185 ATCCAAAGCTTGGTC 1199

RESULT 3

US-09-884-987-1
; Sequence 1, Application US/09884987
; Patent No. US20020102653A1
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu et al
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
; FILE REFERENCE: 0020-4877P
; CURRENT APPLICATION NUMBER: US/09/884,987
; CURRENT FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In/Version 3.0
; SEQ ID NO 1
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: (1831)..(1836)
; NAME/KEY: mat_peptide
; LOCATION: (243)..()
; NAME/KEY: sig_peptide
; LOCATION: (195)..(242)
; NAME/KEY: CDS
; LOCATION: (195)..(1199)
; NAME/KEY: polyA_site
; LOCATION: (2352)..(2357)
; NAME/KEY: polyA_site
; LOCATION: (2516)..(2532)
US-09-884-987-1

Query Match 100.0%; Score 435; DB 10; Length 2534;
Best Local Similarity 100.0%; Pred. No. 1.4e-103;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 60
Db 765 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 824
QY 61 GAATCTCAACCTTAAATCTTGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120
Db 825 GAATCTCAACCTTAAATCTTGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 884
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 180
Db 885 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 944
QY 181 AAGATGCTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 240
Db 945 AAGATGCTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 1004
QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 300
Db 1005 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 1064
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 360
Db 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 1124
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAAATTTCAAACTTCAGAAATGAA 420
Db 1125 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAAATTTCAAACTTCAGAAATGAA 1184

QY 421 ATCCAAAGCTTGGTC 435
|||||
Db 1185 ATCCAAAGCTTGGTC 1199

RESULT 4

US-09-802-669-1
; Sequence 1, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802/669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US/09/668/615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/09/290/640
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221)..(1228)
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 267
; ISSUE: 15
; PAGES: 10709-10715
; DATE: 1992-05-25
; DATABASE ACCESSION NUMBER: X63717/Genbank
; DATABASE ENTRY DATE: 1996-07-19
US-09-802-669-1

Query Match 100.0%; Score 435; DB 10; Length 2551;
Best Local Similarity 100.0%; Pred. No. 1.4e-103;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60
|||||
Db 791 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 850
|||||
QY 61 GAATCTCCAACCTTAATCTGGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120
|||||
Db 851 GAATCTCCAACCTTAATCTGGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 910
|||||
QY 121 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTGA 180
|||||
Db 911 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTGA 970
|||||
QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAAGACACA 240
|||||
Db 971 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAAGACACA 1030
|||||
QY 241 GCAGAACAGAAAGTTCAACTGCTTCGTAATTTGGATCACTTTCATGGAAGAAAGAGCG 300
|||||
Db 1031 GCAGAACAGAAAGTTCAACTGCTTCGTAATTTGGATCACTTTCATGGAAGAAAGAGCG 1090
|||||
QY 301 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAT 360
|||||
Db 1091 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAT 1150
|||||
QY 361 CAGACTATCATCTCAAGGACATTACTAGTACTCAGAAAATTCAGAAATTCAGAAATGAA 420
|||||
Db 1151 CAGACTATCATCTCAAGGACATTACTAGTACTCAGAAAATTCAGAAATTCAGAAATGAA 1210
|||||

QY 421 ATCCAAAGCTTGGTC 435
|||||
Db 1211 ATCCAAAGCTTGGTC 1225

RESULT 5

US-09-966-976A-7/C
; Sequence 7, Application US/09966976A
; Patent No. US20020168649A1
; GENERAL INFORMATION:
; APPLICANT: Ferrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige
; FILE REFERENCE: Secretion and Switch Rearrangement
; FILE REFERENCE: A-66038-4/RMS/JJD/DER
; CURRENT APPLICATION NUMBER: US/09/966/976A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/076/824
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 8282
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-966-976A-7

Query Match 100.0%; Score 435; DB 9; Length 8282;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60
|||||
Db 4353 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 4294
|||||
QY 61 GAATCTCCAACCTTAATCTGGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120
|||||
Db 4293 GAATCTCCAACCTTAATCTGGAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 4234
|||||
QY 121 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTGA 180
|||||
Db 4233 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTGA 4174
|||||
QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAAGACACA 240
|||||
Db 4173 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAAGACACA 4114
|||||
QY 241 GCAGAACAGAAAGTTCAACTGCTTCGTAATTTGGATCACTTTCATGGAAGAAAGAGCG 300
|||||
Db 4113 GCAGAACAGAAAGTTCAACTGCTTCGTAATTTGGATCACTTTCATGGAAGAAAGAGCG 4054
|||||
QY 301 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAT 360
|||||
Db 4053 TATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAT 3994
|||||
QY 361 CAGACTATCATCTCAAGGACATTACTAGTACTCAGAAAATTCAGAAATTCAGAAATGAA 420
|||||
Db 3993 CAGACTATCATCTCAAGGACATTACTAGTACTCAGAAAATTCAGAAATTCAGAAATGAA 3934
|||||
QY 421 ATCCAAAGCTTGGTC 435
|||||
Db 3933 ATCCAAAGCTTGGTC 3919

RESULT 6

US-09-963-206B-7/C
; Sequence 7, Application US/09963206B
; Patent No. US20020123076A1
; GENERAL INFORMATION:

PRIOR FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Version 3.1
SEQ ID NO 8
LENGTH: 8345
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic

US-09-966-976A-8

Query Match 100.0%; Score 435; DB 9; Length 8345;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGAAGCAAGTACAGAAACAATCGAAAAACATCAGAAAACCAGAAAGGAAAAAACCCAAAGCTTCCTCAT 60
Db 4353 AAGAGAAGGAAGTGACAGAAACATCGAAAAACATCGAAAAACGACAGAAAGGAAAAAACCCAAAGCTTCCTCAT 4294
Qy 61 GAATCTCCAACCTTAATACTCGAAACAGTGGCACATAAAATTATCTGTGACTTTGAGTTGAGT 120
Db 4293 GAATCTCCAACCTTAATACTCGAAACAGTGGCAAATAAAATTATCTGTGACTTTGAGTTGAGT 4234
Qy 121 AAATATATACCACTATTTGCTGGAGTCATGCACACTAAGTCAAGTTAAAGCTTTGTTCGA 180
Db 4233 AAATATATACCACTATTTGCTGGAGTCATGCACACTAAGTCAAGTTAAAGCTTTGTTCGA 4174
Qy 181 AGAANTGGTCAATGAAGCCAAANTAGATGAGATCAAGNANTGACAATGCCAAGACACA 240
Db 4173 AGAANTGGTCAATGAAGCCAAANTAGATGAGATCAAGNANTGACAATGCCAAGACACA 4114
Qy 241 GCAGACAGAAAAGCTTCAACTGCTTCTGTAATTGGCACAACCTTCATGGAAGAAAGGCG 300
Db 4113 GCAGACAGAAAAGCTTCAACTGCTTCTGTAATTGGCACAACCTTCATGGAAGAAAGGCG 4054
Qy 301 TATGACACATGTATTAAAGATCTCAAAAAGCCAACTTTTGTACTCTTCGACAGAAAAAT 360
Db 4053 TATGACACATGTATTAAAGATCTCAAAAAGCCAACTTTTGTACTCTTCGACAGAAAAAT 3994
Qy 361 CAGACTATCATCTCAAGNACATTAAGTAGTGTGACTCAGAAAAATTCAAACTTCAGAAATGAA 420
Db 3993 CAGACTATCATCTCAAGNACATTAAGTAGTGTGACTCAGAAAAATTCAAACTTCAGAAATGAA 3934

Qy 421 ATCCAAAGCTTGTC 435
Db 3933 ATCCAAAGCTTGTC 3919

RESULT 8
US-09-963-206B-8/c
Sequence 8, Application US/09963206B
Patent No. US20020123076A1
GENERAL INFORMATION:
APPLICANT: Ferrick, David A.
APPLICANT: Swift, Susan E.
APPLICANT: Armstrong, Randall
APPLICANT: Fox, Bryan
TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and
FILE REFERENCE: Secretion and Switch Rearrangement
CURRENT APPLICATION NUMBER: US/09/963, 206B
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US /09/076, 624
PRIOR FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In version 3.1
SEQ ID NO 8
LENGTH: 8345
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic

US-09-963-206B-8

Db	122	GAATCTCCAACTT	TAGATCTCCTGAAACAGACAGAGGCAATAAATTTATCTGATGTTTGACCTTGACT	181
Qy	121	AAATATATACCACT	ATTGCTGGAGTCAATGACACATAAGCTCAAGTTAAAGGCTTTGTTCTCGA	180
Db	182	AAATATATACCACT	ATTGCTGGAGTCAATGACACATAAGCTCAAGTTAAAGGCTTTGTTCTCGA	241
Qy	181	AAGAAATGGTGTCA	ATGAAGCCAAATAGATCAGATCAAGAATGACAATGTCCACAGACACA	240
Db	242	AGAATGGTGTCAAT	GAAGCCAAATAGATGAGATCAAGAATGACAATGTCCAGACACA	301
Qy	241	GCAGACAGAAAAGT	TCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCG	300
Db	302	GCAGACAGAAAAGT	GCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCG	361
Qy	301	TATGACACATTGAT	TAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAAAT	360
Db	362	TATGACACATTGAT	TAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAAAT	421
Qy	361	CAGACTATCATCTC	CAAGGACATTACTAGTACTCAGAAAAATTCAAACTTCAGAAATGAA	420
Db	422	CAGACTATCATCTC	CAAGGACATTACTAGTACTCAGAAAAATTCAAACTTCAGAAATGAA	481
Qy	421	ATCCAAAGC	429	
Db	482	ATCCAAAGC	490	
RESULT 10				
US-09-867-701-2490				
: Sequence 2490, Application US/09867701				
: Patent No. US2002013237A1				
: GENERAL INFORMATION:				
: APPLICANT: Aglate, Paul A.				
: APPLICANT: Jones, Robert				
: APPLICANT: Harlocker, Susan L.				
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY				
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER				
: FILE REFERENCE: 210121.497				
: CURRENT APPLICATION NUMBER: US/09/867,701				
: CURRENT FILING DATE: 2001-05-29				
: NUMBER OF SEQ ID NOS: 10912				
: SOFTWARE: FastSeq for Windows Version 4.0				
: SEQ ID NO 2490				
: LENGTH: 398				
: TYPE: DNA				
: ORGANISM: Homo sapien				
: FEATURE:				
: NAME/KEY: misc_feature				
: LOCATION: (1)...(398)				
: OTHER INFORMATION: n = A,T,C or G				
US-09-867-701-2490				
Query Match 90.7%; Score 394.4; DB 10; Length 398;				
Best Local Similarity 99.5%; Pred. No. 2.2e-93;				
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0				
Qy	32	AGCACAGAAAGGAAA	ACCAGGTTCTCATGAACTTCCAACTTAAATCCTGAAACAGTGG	91
Db	1	AGCACAGAAAGGAAA	ACCAGGTTCTCATGAACTTCCAACTTAAATCCTGAAACAGTGG	60
Qy	92	CAATAAATTTATCT	GTGAGTTGAGTAAATATATACCACTATTGCTGGAGTCATGA	151
Db	61	CAATAAATTTATCT	GTGAGTTGAGTAAATATATACCACTATTGCTGGAGTCATGA	120
Qy	152	CACTAAGTCRAAGT	TAAAGGCTTTGTTTGGAAAGATGGTGTCAATCAAGCCCAAAATAGATG	211
Db	121	CACTAAGTCRAAGT	TAAAGGCTTTGTTTGGAAAGATGGTGTCAATCAAGCCCAAAATAGATG	180
Qy	212	AGATCAAGAATGACA	ATGTCCAAAGACACAGCAGAAAGTTTCAACTGCTTCCTGAATT	271
Db	181	AGATCAAGAATGACA	ATGTCCAAAGACACAGCAGAAAGTTTCAACTGCTTCCTGAATT	240
Qy	272	GGCATCAACTTCAT	GGAAGAAAGGCGTATGACACATTTGATTAAAGATCTCAAAAAG	331

Db 241 GCATCAACTTCATGGAAGAAGCGTATGACACATTGATTAAAGATCTCAAAAAAG 300
QY 332 CCAATCTTTGTACTCTTGAGAGAAAAATTCAGACTATCATCTCAAGGACATTACTAGTG 391
Db 301 CCAATCTTTGTACTCTTGAGAGAAAAATTCAGACTATCATCTCAAGGACATTACTAGTG 360
QY 392 ACTCAGAAAATTCAAACTTCAGAAATGAAATCCAAAG 428
Db 361 ACTCGAAAAATTCAAANCITTCAGAAATGAAATCCAAAG 397

RESULT 11

US-09-867-701-3156
; Sequence 3156, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND/DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 2001-05-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3156
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3156

Query Match 88.2%; Score 383.6; DB 10; Length 460;
Best Local Similarity 99.0%; Pred. No. 1.6e-90;
Matches 386; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 46 AACCAAGGTTCTCATGAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCT 105
Db 1 AACCAAGGTTCTCATGAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCT 60
QY 106 GATGTTGACTTGAGTAAATATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTT 165
Db 61 GATGTTGACTTGAGTAAATATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTT 120
QY 166 AAAGGCTTTGTCGAAGAAGTGGTCTCAATGAAGCCAAATAGATGAGATCAAGATGAC 225
Db 121 AAAGGCTTTGTCGAAGAAGTGGTCTCAATGAAGCCAAATAGATGAGATCAAGATGAC 180
QY 226 AATGTCGAAGACACAGCAGAGAAAGTTCAACTGCTTCGTTAAATGGCATCAACTTCAT 285
Db 181 AATGTCGAAGACACAGCAGAGAAAGTTCAACTGCTTCGTTAAATGGCATCAACTTCAT 240
QY 286 GGAAGAAGAAGCGTATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACT 345
Db 241 GGAAGAAGAATATCGTATGACACATTGATTAAAGATCTCAAAAAAGCCAATCTTTGTACT 300
QY 346 CTTCGAGAGAAATTCAGACTATCATCTCAAGGACATTACTAGTGCATCAGAAAATTC 405
Db 301 CTTCGAGAGAAATTCAGACTATCATCTCAAGGACATTACTAGTGCATCAGAAAATTC 360
QY 406 AACTTCAGAAATGAAATCCAAAGCTTGGTC 435
Db 361 AACTTCAGAAATGAAATCCAAAGCTTGGTC 390

RESULT 12

US-09-954-531-998
; Sequence 998, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 998
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-998
Query Match 81.4%; Score 354; DB 9; Length 975;
Best Local Similarity 100.0%; Pred. No. 1.2e-82;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATATACCACTATTGCT 141
Db 485 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATATACCACTATTGCT 544
QY 142 GGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCCGAAAGAAATGGTGTCAATGAAGCC 201
Db 545 GGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCCGAAAGAAATGGTGTCAATGAAGCC 604
QY 202 AAATAGATGAGATCAAGATGACAATGTCCAAAGACACAGCAGACAGAAAGTTCAACTG 261
Db 605 AAATAGATGAGATCAAGATGACAATGTCCAAAGACACAGCAGACAGAAAGTTCAACTG 664
QY 262 CTTCGTAATGGCATCAACTTCATGGAAGAAGGCGTATGACACATTGATTAAAGAT 321
Db 665 CTTCGTAATGGCATCAACTTCATGGAAGAAGGCGTATGACACATTGATTAAAGAT 724
QY 322 CTCAAAAAGCAACTCTTTGTACTCTTCGAGAGAAAATTCAGACTATCATCTCAAGGAC 381
Db 725 CTCAAAAAGCAACTCTTTGTACTCTTCGAGAGAAAATTCAGACTATCATCTCAAGGAC 784
QY 382 ATTACTAGTACTCAGAAAATTCAAACTTCAGAAAATGAAATCCAAAGCTTGGTC 435
Db 785 ATTACTAGTACTCAGAAAATTCAAACTTCAGAAAATGAAATCCAAAGCTTGGTC 838

RESULT 13

US-09-802-669-101
; Sequence 101, Application US/09802669
; Patent No. US2002000490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US/09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 1840
; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (95)...(426)
US-09-802-669-101

Query Match
Best Local Similarity 75.9%; Score 330; DB 10; Length 1840;
Matches 333; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 98 ATTATCTGATGTTGACCTTGAAGTAATATATACACACATATGCTGGAGTCATGACACTAA 157
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DB 86 ATTTTCAGATGTTGACCTTGTGTAATATATACACACATATGCTGGAGTCATGCTACTAT 145
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QY 158 GTCAAGTTAAAGGCTTTGTTGAAAGATGTGTCAATGAAGCCAAAATAGATGAGATCA 217
|||||
DB 146 GTCAAGTTAAAGGCTTTGTTGAAAGATGTGTCAATGAAGCCAAAATAGATGAGATCA 205
|||||

QY 218 AGAATGACAAATGTCACACACACAGCAGACAGAAAGTTCAACTGCTTGTGTAATGGCATC 277
|||||
DB 206 AGAATGACAAATGTCACACACACAGCAGACAGAAAGTTCAACTGCTTGTGTAATGGCATC 265
|||||

QY 278 AACTTCATGGAAGAAAGCGTATGACACATTCATTAAAGATCTCAAAAAAGCCAATC 337
|||||
DB 266 AACTTCATGGAAGAAAGCGTATGACACATTCATTAAAGATCTCAAAAAAGCCAATC 325
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QY 338 TTGTACTCTTCGACAGAAAATTCAGACTATCATCTCAAGGACATTAATAGTACTAGTCA 397
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DB 326 TTGTACTCTTCGACAGAAAATTCAGACTATCATCTCAAGGACATTAATAGTACTAGTCA 385
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QY 398 AAAATTCAACTTCAGAAATGAATCCAAAGCTTGGTC 435
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DB 386 AAAATTCAACTTCAGAAATGAATCCAAAGCTTGGTC 423
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RESULT 14
US-09-918-995-13045
; Sequence 13045, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13045
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(489)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-13045

Query Match
Best Local Similarity 69.4%; Score 302; DB 9; Length 489;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 CTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGAAAGATGCTGTC 193
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DB 55 CTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGAAAGATGCTGTC 114
|||||

QY 194 ATGAAGCCAAAATAGATGAGATCAAGATGACAATGTCCAAGACACAGCAGAACAGAAAG 253
|||||
DB 115 ATGAAGCCAAAATAGATGAGATGACAATGTCCAAGACACAGCAGAACAGAAAG 174
|||||

QY 254 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGCGTATGACACATTGA 313
|||||

Db 175 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCGTATGACACATTGA 234
|||||

QY 314 TTAAGATCTCAAAAAAGCCAAATCTTTGTACTCTTTCGACAGAGAAATTCAGACTATCATCC 373
|||||

Db 235 TTAAGATCTCAAAAAAGCCAAATCTTTGTACTCTTTCGACAGAGAAATTCAGACTATCATCC 294
|||||

QY 374 TCAAGGACATTTACTAGTACTGACTCAGAAAATTTCAAATTCAGAAATGAAATCCAAAAGCTTGG 433
|||||

Db 295 TCAAGGACATTTACTAGTACTGACTCAGAAAATTTCAAATTCAGAAATGAAATCCAAAAGCTTGG 354
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QY 434 TC 435
||

Db 355 TC 356
||

RESULT 15
US-09-918-995-15171
; Sequence 15171, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15171
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(496)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15171

Query Match
Best Local Similarity 69.4%; Score 302; DB 9; Length 496;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 CTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGAAAGATGCTGTC 193
|||||

Db 63 CTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTCGAAAGATGCTGTC 122
|||||

QY 194 ATGAAGCCAAAATAGATGAGATCAAGATGACAATGTCCAAGACACAGCAGAACAGAAAG 253
|||||

Db 123 ATGAAGCCAAAATAGATGAGATCAAGATGACAATGTCCAAGACACAGCAGAACAGAAAG 182
|||||

QY 254 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGCGTATGACACATTGA 313
|||||

Db 183 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGCGTATGACACATTGA 242
|||||

QY 314 TTAAGATCTCAAAAAAGCCAAATCTTTGTACTCTTTCGACAGAGAAATTCAGACTATCATCC 373
|||||

Db 243 TTAAGATCTCAAAAAAGCCAAATCTTTGTACTCTTTCGACAGAGAAATTCAGACTATCATCC 302
|||||

QY 374 TCAAGGACATTTACTAGTACTGACTCAGAAAATTTCAAATTCAGAAATGAAATCCAAAAGCTTGG 433
|||||

Db 303 TCAAGGACATTTACTAGTACTGACTCAGAAAATTTCAAATTCAGAAATGAAATCCAAAAGCTTGG 362
|||||

QY 434 TC 435
||

Db 363 TC 364
||

Search completed: June 15, 2003, 22:03:40
Job time : 134 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 19:50:58 ; Search time 1424 Seconds
(without alignments)
4947.357 Million cell updates/sec

Title: US-09-884-987-1_COPY_765_1199

Perfect score: 435

Sequence: 1 aagagaaggaggtacagaa.....atgaataccaagcttggtc 435

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	433.4	99.6	509	10 AW994695	AW994695 RC1-BN003
2	429.8	98.8	1055	14 BQ051037	BQ051037 AGENCOURT
3	412	94.7	776	13 B1254532	B1254532 602978522
4	406.4	93.4	809	12 BF126149	BF126149 601650407
5	394.4	90.7	398	9 AA180032	AA180032 z093g12.r
6	383.6	88.2	460	9 AA293570	AA293570 zt25h11.r

7	370	85.1	676	14 W05802	W05802 za89f05.r1
8	354	81.4	417	10 AV651157	AV651157 AV651157
9	297.8	68.5	395	10 BE070451	BE070451 QV4-BF040
10	286	65.7	305	9 AA860068	AA860068 HGBBT125
11	264.2	60.7	1152	14 BM922638	BM922638 AGENCOURT
12	201.2	46.3	696	10 AV715411	AV715411 AV715411
13	196.4	45.1	217	9 AA852070	AA852070 HGBBT116
14	172	39.5	461	14 H02935	H02935 yj48b08.r1
15	169.4	38.9	932	9 AL542093	AL542093 AL542093
16	167.6	38.5	1437	11 AK002590	AK002590 Mus muscu
17	161	37.0	954	9 AA745982	AA745982 obi18q12.s
18	154.4	35.5	735	13 B1766250	B1766250 603053708
19	147.8	34.0	663	10 AW141748	AW141748 EST291827
20	89.6	20.6	827	9 AJ392468	AJ392468 AJ392468
21	60.6	13.9	646	9 AL542092	AL542092 AL542092
22	53	12.2	963	9 AL566565	AL566565 AL566565
23	47.2	10.9	996	17 CNS00FUH	AL071063 Drosoph11
24	47	10.8	523	13 BJ441951	BJ441951 BJ441951
25	46.4	10.7	642	13 BJ436174	BJ436174 BJ436174
26	46.2	10.6	473	13 BJ379111	BJ379111 BJ379111
27	45	10.3	782	17 AZ175342	AZ175342 SE_0132_A
28	44.8	10.3	584	9 AT231531	AT231531 EST228219
29	44.8	10.3	695	17 AZ318375	AZ318375 IM0037N07
30	44.8	10.3	706	13 BJ345089	BJ345089 BJ345089
31	44.2	10.2	500	13 BJ363187	BJ363187 BJ363187
32	44	10.1	290	14 C90546	C90546 C90546 Dict
33	43.8	10.1	482	13 BJ413360	BJ413360 BJ413360
34	43.8	10.1	528	13 BJ360248	BJ360248 BJ360248
35	43.8	10.1	531	13 BJ389689	BJ389689 BJ389689
36	43.8	10.1	539	13 BJ364065	BJ364065 BJ364065
37	43.8	10.1	559	13 BJ387004	BJ387004 BJ387004
38	43.8	10.1	563	13 BJ324059	BJ324059 BJ324059
39	43.8	10.1	564	13 BJ388447	BJ388447 BJ388447
40	43.8	10.1	567	13 BJ323809	BJ323809 BJ323809
41	43.8	10.1	568	13 BJ391376	BJ391376 BJ391376
42	43.8	10.1	571	13 BJ328095	BJ328095 BJ328095
43	43.8	10.1	571	13 BJ414027	BJ414027 BJ414027
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ALIGNMENTS

RESULT 1
AW994695

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

AW994695 RC1-BN0039-060200-011-a05 BN0039 Homo sapiens CDNA, mRNA sequence.
509 bp linear EST 05-JUN-2000

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AW994695 RC1-BN0039-060200-011-a05 BN0039 Homo sapiens CDNA, mRNA sequence.

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC1-BN0039-060
200-011-a056t3-2000-02-066t4-1)
Seq primer: puc.18 forward
High quality sequence stop: 509.
Location/Qualifiers

FEATURES

source
1..509
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0039"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
205 a 83 c 99 g 122 t

BASE COUNT
ORIGIN

Query Match 99.6%; Score 433.4; DB 10; Length 509;
Best Local Similarity 99.8%; Pred. No. 5.1e-91;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 60
|||||
DB 17 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 76
|||||
QY 61 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
|||||
DB 77 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 136
|||||
QY 121 AAATATATCATCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 180
|||||
DB 137 AAATATATCATCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 196
|||||
QY 181 AAGAAAGGTTCTCAATGAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 240
|||||
DB 197 AAGAAAGGTTCTCAATGAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 256
|||||
QY 241 GCAGACAGAAAGTTCAACTGCTTCTGTAATGGCATCACTTCAATGAGAAAGAAAGCG 300
|||||
DB 257 GCAGACAGAAAGTTCAACTGCTTCTGTAATGGCATCACTTCAATGAGAAAGAAAGCG 316
|||||
QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 360
|||||
DB 317 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 376
|||||
QY 361 CAGACTATCATCTCAAGGACATTAAGTACTGACATGAGAAATTCAAACTTCAGAAATGAA 420
|||||
DB 377 CAGACTATCATCTCAAGGACATTAAGTACTGACATGAGAAATTCAAACTTCAGAAATGAA 436
|||||
QY 421 ATCCAAAGCTTGCTC 435
|||||
DB 437 ATCCAAAGCTTGCTC 451
|||||

RESULT 2.
BO051037 1055 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT_6954504 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5785846
5', mRNA sequence.

ACCESSION
VERSION
BO051037
KEYWORDS
EST.
SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1055)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaos@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12873 row: j column: 23
High quality sequence stop: 689.
Location/Qualifiers

FEATURES
source

1..1055
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
352 a 221 c 215 g 267 t

BASE COUNT
ORIGIN

Query Match 98.8%; Score 429.8; DB 14; Length 1055;
Best Local Similarity 99.5%; Pred. No. 3.9e-90;
Matches 431; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 60
|||||
DB 374 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 433
|||||
QY 61 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
|||||
DB 434 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 493
|||||
QY 121 AAATATATCATCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 180
|||||
DB 494 AAATATATCATCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 553
|||||
QY 181 AAGAAAGGTTCTCAATGAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 240
|||||
DB 554 AAGAAAGGTTCTCAATGAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 613
|||||
QY 241 GCAGACAGAAAGTTCAACTGCTTCTGTAATGGCATCACTTCAATGAGAAAGAAAGCG 300
|||||
DB 614 GCAGACAGAAAGTTCAACTGCTTCTGTAATGGCATCACTTCAATGAGAAAGAAAGCG 673
|||||
QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 360
|||||
DB 674 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 733
|||||
QY 361 CAGACTATCATCTCAAGGACATTAAGTACTGACATGAGAAATTCAAACTTCAGAAATGAA 420
|||||
DB 734 CAGACTATCATCTCAAGGACATTAAGTACTGACATGAGAAATTCAAACTTCAGAAATGAA 793
|||||
QY 421 ATCCAAAGCTTGCTC 433
|||||
DB 794 ATCCAAAGCTTGCTC 806
|||||

RESULT 3
BI254532

LOCUS
DEFINITION
BI254532
ACCESSION
VERSION
BI254532.1
KEYWORDS
EST.

BI254532 776 bp mRNA linear EST 17-JUL-2001
602978522F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123477 5',
mRNA sequence.
BI254532
VERSION
BI254532.1 GI:114807044
KEYWORDS
EST.


```

SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 776)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cspab@remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: Incyte Genomics, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L14M1301 row: 1 column: 06
            High quality sequence stop: 757.

FEATURES   Location/Qualifiers
            1..776
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="MGC_12"
             /tissue_type="cervical carcinoma cell line"
             /lab_host="DH10B"
             /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
             Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
             Average insert size 1.4 kb. Library prepared by Life
             Technologies."
BASE COUNT 276 a 136 c 151 g 213 t
ORIGIN
Query Match      94.7%; Score 412; DB 13; Length 776;
Best Local Similarity 99.5%; Pred. No. 5.3e-86;
Matches 434; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 AAGAGAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGTTCTCAT 60
DB 102 AAGAGAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGTTCTCAT 161
QY 61 GAATCTCCACCTTAAATCTGGAACAGTGCGCAATAAATTTATCTGATGTTGACTTGAG 119
DB 162 GAATCTCCACCTTAAATCTGGAACAGTGCGCAATAAATTTATCTGATGTTGACTTGAG 221
QY 120 TAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTG 179
DB 222 TAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTCAAGGCTTTGTTG 280
QY 180 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCCAGACAC 239
DB 281 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCCAGACAC 340
QY 240 AGCAGACAGAAAGTTCACCTGCTTCGTAATGTCATCACTTCACTGATGAAAGAAAGC 299
DB 341 AGCAGACAGAAAGTTCACCTGCTTCGTAATGTCATCACTTCACTGATGAAAGAAAGC 400
QY 300 GTATGACACATTTGATTAAGATCTCAAAAAGGCAAACTTTGTAATCTTGCAGAGAAAT 359
DB 401 GTATGACACATTTGATTAAGATCTCAAAAAGGCAAACTTTGTAATCTTGCAGAGAAAT 460
QY 360 TCAGACTATCATCTCAAGGACATTTAGTGACTCAGAAAATTCAAACTTCAGAAATGA 419
DB 461 TCAGACTATCATCTCAAGGACATTTAGTGACTCAGAAAATTCAAACTTCAGAAATGA 520
QY 420 AATCCAAGCTTGTC 435
DB 521 AATCCAAGCTTGTC 536

us-09-884-987-1-copy_765_1199.rst
LOCUS      BF126149
DEFINITION 601650407F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:3934273 5',
            mRNA sequence.
ACCESSION  BF126149
VERSION     BF126149.1 GI:10965189
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 809)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cspab@remail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            CDNA Library Preparation: CLONTECH Laboratories, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM774 row: n column: 02
            High quality sequence stop: 635.

FEATURES   Location/Qualifiers
            1..809
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="NIH_MGC_76"
             /lab_host="DH10B (T1 phage-resistant)"
             /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
             SfiI (ggcccttcgccc); Site_2: SfiI (ggccattatggccc); 5' and
             3' adaptors were used in cloning as follows: 5' adaptor
             sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
             5'-ATCTAGAGCCGAGCGCGGACATG-dt(30)BN-3' (where B = A,
             C, or G and N = A, C, G, or T). Average insert size 1.85
             kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
             by PCR. This library was enriched for full-length clones
             and was constructed by Clontech Laboratories (Palo Alto,
             CA). Note: this is a NIH_MGC Library."
BASE COUNT 293 a 127 c 179 g 210 t
ORIGIN
Query Match      93.4%; Score 406.4; DB 12; Length 809;
Best Local Similarity 99.3%; Pred. No. 1.1e-84;
Matches 429; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 1 AAGAGAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGTTCTCAT 60
DB 87 AAGAGAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGTTCTCAT 146
QY 61 GAATCTCCACCTTAAATCTGGAACAGTGCGCAATAAATTTATCTGATGTTGACTTGAGT 120
DB 147 GAATCTCCACCTTAAATCTGGAACAGTGCGCAATAAATTTATCTGATGTTGACTTGAGT 206
QY 121 AATATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180
DB 207 AATATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 265
QY 181 AAGATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCCAGACACA 240
DB 266 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCCAGACACA 325
QY 241 GCAGAACAGAAAGTTCACCTGCTTCGTAATGTCATCACTTCACTGATGAAAGAAAGC 300
DB 326 GCAGAACAGAAAGTTCACCTGCTTCGTAATGTCATCACTTCACTGATGAAAGAAAGC 385
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGGCAAACTTTGTAATCTTGCAGAGAAAT 360
DB 386 TATGACACA-TGATTAAGATCTCAAAAAGGCAAACTTTGTAATCTTGCAGAGAAAT 444
RESULT 4
BF126149
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361 CAGACTATCATCTCCTCAAGGACATTTACTAGTCTCAGAAATTCAGAAATGAA 420
|||||
445 CAGACTATCATCTCCTCAAGGACATTTACTAGTCTCAGAAATTCAGAAATGAA 504
|||||
421 ATCCAAAGCTTG 432
|||||
505 ATCCAAAGCTGG 516

RESULT 5
AA180032 398 bp mRNA linear EST 31-DEC-1996
LOCUS z093g12.r1 Stratagene ovarian cancer (#937219) Homo sapiens CDNA
DEFINITION clone IMAGE:594502 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA180032
VERSION AA180032.1 GI:1761298
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 398)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
CONTACT: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 from Amersham
High quality sequence stop: 263.
Location/Qualifiers
1. 398
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:594502"
/clone_lib="Stratagene ovarian cancer (#937219)"
/sex="female"
/dev_stage="adult, 64 years"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Cloned unidirectionally. Primer: Oligo dt. Papillary
serous carcinoma, isolated from ascites, 64 year old
caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTT 3'"
BASE COUNT 155 a 73 c 73 g 96 t 1 others
ORIGIN
Query Match 90.7%; Score 394.4; DB 9; Length 398;
Best Local Similarity 99.5%; Pred. No. 6,1e-82;
Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

32 AGCAGAGAAAGAAACCAAGGTTCTCATGAAATCTCCAAACCTTAATCTCGAAGAGTGG 91
|||||
1 AGCAGAGAAAGAAACCAAGGTTCTCATGAAATCTCCAAACCTTAATCTCGAAGAGTGG 60
|||||
92 CAATAAATTTACTGATGTTGACTTTCAGTAATATATACCACTATTCTGCGAGTCATGA 151
|||||
61 CAATAAATTTACTGATGTTGACTTTCAGTAATATATATACCACTATTCTGCGAGTCATGA 120
|||||
152 CACTAAGTCAAGTTAAAGGCTTTGTTTCGAAAGAAATGGTGTCTCAATGAAGCCAAATAGATG 211
|||||

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121 CACTAAGTCAAGTTAAAGGCTTTGTTTCGAAAGAAATGGTGTCTCAATGAAGCCAAATAGATG 180
|||||
212 AGATCAAGAAATGACAAATGTCCTCAAGACACAGACAGAAAGTTCAACTGCTTCGTAATT 271
|||||
181 AGATCAAGAAATGACAAATGTCCTCAAGACACAGACAGAAAGTTCAACTGCTTCGTAATT 240
|||||
272 GGCATCAACTTTCATGGAAGAAAGCGGTATGACACATTTGATTAAGATCTCAAAAAG 331
|||||
241 GGCATCAACTTTCATGGAAGAAAGCGGTATGACACATTTGATTAAGATCTCAAAAAG 300
|||||
332 CCAATCTTTTGTACTCTTTCAGAGAGAAATTCAGACTATCATCTCAAGAGCATTTACTAGTG 391
|||||
301 CCAATCTTTTGTACTCTTTCAGAGAGAAATTCAGACTATCATCTCAAGAGCATTTACTAGTG 360
|||||
392 ACTCAGAAAATTCAAACTTCAGAAATGAAATCCAAAG 428
|||||
361 ACTCGGAAAATTCAAACTTCAGAAATGAAATCCAAAG 397
|||||

RESULT 6
AA293570 460 bp mRNA linear EST 08-AUG-1997
LOCUS zt25h11.r1 Soares ovary tumor NbHOT Homo sapiens CDNA clone
DEFINITION IMAGE:714213 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN)
); mRNA sequence.
ACCESSION AA293570
VERSION AA293570.1 GI:1941237
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
CONTACT: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1853 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 125.
Location/Qualifiers
1. 460
/organism="Homo sapiens"
/db_xref="GDB:5934710"
/db_xref="taxon:9606"
/clone="IMAGE:714213"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: p7T7D3 (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T7 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
TITLE JOURNAL
MEDLINE
COMMENT
FEATURES
SOURCE

```

```
BASE COUNT 175 a 80 c 81 g 124 t
ORIGIN
Query Match 88.2%; Score 383.6; DB 9; Length 460;
Best Local Similarity 99.0%; Pred. No. 2.1e-79;
Matches 386; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 46 AACCAAGGTTTCATGATCTCCACCTTAATCTGGAACAGTGGCAATAATTTATCT 105
DB 1 AACCAAGGTTTCATGATCTCCACCTTAATCTGGAACAGTGGCAATAATTTATCT 60
QY 106 GATGTTGACTTCAGTAAATATATACCACTATTGCTGGAGTCATGACATCAAGTTC 165
DB 61 GATGTTGACTTCAGTAAATATATACCACTATTGCTGGAGTCATGACATCAAGTTC 120
QY 166 AAAGGCTTTGTTGCGAAGAAATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGAC 225
DB 121 AAAGGCTTTGTTGCGAAGAAATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGAC 180
QY 226 ATGTCCACAGACAGACAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCAT 285
DB 181 ATGTCCACAGACAGACAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCAT 240
QY 286 GGAAGAAAGAGCGCTATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACT 345
DB 241 GGAAGAAATATCTGATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACT 300
QY 346 CTTGCAGAGAAATTCAGACTATCATCTCTCAAGGACATTTAGTGACTCAGAAATTCATCA 405
DB 301 CTTGCAGAGAAATTCAGACTATCATCTCTCAAGGACATTTAGTGACTCAGAAATTCATCA 360
QY 406 AACTTCAGAAATGAATCAAAAGCTTGGTC 435
DB 361 AACTTCAGAAATGAATCAAAAGCTTGGTC 390

RESULT 7
W05802 676 bp mRNA linear EST 23-APR-1996
LOCUS za89f05.r1 Soares_fetal_lung_NBHL19W Homo. sapiens cDNA clone
DEFINITION IMAGE:299745 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
); mRNA sequence.
ACCESSION W05802.1 GI:1278534
VERSION W05802.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
R., Williamson, A., Woldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson-RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 307.
Location/Qualifiers
1. .676
/organism="Homo sapiens"
/db_xref="GDB:1244669"
/db_xref="taxon:9606"
/clone="IMAGE:299745"
/clone_lib="Soares_fetal_lung_NBHL19W"

FEATURES
source
```

```
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."
BASE COUNT 231 a 127 c 138 g 171 t 9 others
ORIGIN
Query Match 85.1%; Score 370; DB 14; Length 676;
Best Local Similarity 98.0%; Pred. No. 3.2e-76;
Matches 395; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 3 GAGAAAGGAAGTACAGAAAACATGCGAAGAGCAGACAGAAAGGAAAGGTTCTCATCA 62
DB 16 GAGAAAGGAAGTACAGAAAACATGCGAAGAGCAGACAGAAAGGAAAGGTTCTCATCA 75
QY 63 ATCTCAACCTTAAATCTGAAACAGTGGCAATAATTTATCTGATGTTGACTTCAGTAA 122
DB 76 ATCTCAACCTTAAATCTGAAACAGTGGCAATAATTTATCTGATGTTGACTTCAGTAA 135
QY 123 ATATATCACCCTATTGCTGGAGTCATGACACATAGTCAAGTTAAAGGCTTTGTT 181
DB 136 ATATATCACCCTATTGCTGGAGTCATGACACATAGTCAAGTTAAAGGCTTTGTT 195
QY 182 AGAATGGTCTCAATGAAGCCAAATAGATGATCAAGAAATGCAATGCAAGACACAG 241
DB 196 AGAATGGTCTCAATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGAT 255
QY 242 CAGACAGAAAGTTCACACTGCTT-CGTAAATGGCATCAACTTCATGGAAGAAAGGCG 300
DB 256 CAGACAGAAAGTTCACACTGCTT-CGTAAATGGCATCAACTTCATGGAAGAAAGGCG 315
QY 301 TATGACACATTCATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTCGACAGAAAT 360
DB 316 TATGACACATTCATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTCGACAGAAAT 375
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTCAAGTCAAGAAAT 403
DB 376 CAGACTATCATCTCAAGGACATTTACTAGTCAAGTCAAGAAAT 418

RESULT 8
AV651157 417 bp mRNA linear EST 15-JAN-2002
LOCUS AV651157 GLC Homo sapiens cDNA clone GLCCMD03 3', mRNA sequence.
DEFINITION AV651157
ACCESSION AV651157
VERSION AV651157.1 GI:9872171
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
```

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel.: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

source
 1. .417
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GLCCMD03"
 /clone_lib="GLC"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 151 a 74 c 84 g 108 t
 ORIGIN

Query Match .81.4%; Score 354; DB 10; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.6e-72;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60
 DB 64 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 123
 QY 61 GAATCTCAACCTTAAATCTGAAACAGTGCATTAATTTATCTGATGCTTGCAT 120
 DB 124 GAATCTCAACCTTAAATCTGAAACAGTGCATTAATTTATCTGATGCTTGCAT 183
 QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180
 DB 184 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 243
 QY 181 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 240
 DB 244 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 303
 QY 241 GCAGAACAGAAAGTCAACTGCTCGTAATGGCATCAACTTCTTACTCTTGCAGAG 354
 DB 364 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAG 417

RESULT 9
 BE070451/c 395 bp mRNA linear EST 09-JUN-2000
 LOCUS
 DEFINITION QV4-BT0407-020300-122-d09 BT0407 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE070451
 VERSION BE070451.1 GI:8415097
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 395)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 LABORATORY: Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 http://www.ludwig.org.br/scripts/gethtml2.pl?l1=5t2-QV4-BT0407-020
 300-122-d09&l3=2000-03-02&l4=1)

Seq primer: puc 18 forward
 High quality sequence start: 50
 High quality sequence stop: 395.

FEATURES

source
 1. 395
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BT0407"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 103 a 81 c 67 g 144 t
 ORIGIN

Query Match .68.5%; Score 297.8; DB 10; Length 395;
 Best Local Similarity 95.5%; Pred. No. 2e-59;
 Matches 318; Conservative 0; Mismatches 12; Indels 3; Gaps 1;
 QY 1 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60
 DB 336 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 277
 QY 61 GAATCTCAACCTTAAATCTGAAACAGTGCATTAATTTATCTGATGCTTGCAT 120
 DB 276 GAATCTCAACCTTAAATCTGAAACAGTGCATTAATTTATCTGATGCTTGCAT 217
 QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180
 DB 216 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 157
 QY 181 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 240
 DB 156 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACA 97
 QY 241 GCAGAACAGAAAGTCAACTGCTCGTAATGGCATCAACTTCTTGCAGAA---AGAAAGAA 297
 DB 96 GCAGAACAGAAAGTCAACTGCTCGTAATGGCATCAACTTCTTGCAGAAAGGAAAG 37
 QY 298 GCGTATGACACATTGATTAAAGATCTCAAAAAA 330
 DB 36 TAGTATGACACATTGATTAAAGATCTCAATAA 4

RESULT 10
 AA860068 305 bp mRNA linear EST 11-MAR-1998
 LOCUS HGBBT125 Human Glioblastoma Cell Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION AA860068
 VERSION AA860068.1 GI:2952547
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 305)
 Jlin, H.L., Hu, S.N., Tu, C., Yuan, J.G. and Qiang, B.Q.
 DDRT-PCR of Human Glioblastoma Cell Line BT-325 CDNA
 Unpublished (1997)

COMMENT

Contact: Boqin Qiang
National Laboratory of Medical Molecular Biology, CAMS & PUMC
Institute of Basic Medical Sciences, Peking Union Medical College &
Chinese Academy of Medical Sciences
5 Dong Dan Tiao, Beijing 100005, P.R. China
Tel: (010)65296411
Fax: 8610-5240529
Email: zh357@iname.com

Seq primer: M13 Reverse Primer.

FEATURES

source

Location/Qualifiers

1..305
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human Glioblastoma Cell"
/cell_type="Glioblastoma Cell"
/cell_lines="BT-325"
/lab_host="E.coli DH5a"

/note="Organ: Brain; Vector: PCR11, Invitrogen; Total RNA was isolated from human glioblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell. Differentially expressed PCR products were cloned and sequenced."

BASE COUNT 122 a 52 c 64 g 67 t

ORIGIN

Query Match 65.7%; Score 286; DB 9; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.1e-56;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 60
DB 20 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 79
QY 61 GAATCTCCAACTTAATCTTGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 120
DB 80 GAATCTCCAACTTAATCTTGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 139
QY 121 AAATATATCACACATATTGCTGGAGTCATGACATCAAGTTAAAGGCTTTGTCGA 180
DB 140 AAATATATCACACATATTGCTGGAGTCATGACATCAAGTTAAAGGCTTTGTCGA 199
QY 181 AAGATGCTGTCATGAGCCAAATAGATCAGATCAAGATCAAGTGTCCACACACA 240
DB 200 AAGATGCTGTCATGAGCCAAATAGATCAGATCAAGATCAAGTGTCCACACACA 259
QY 241 GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATG 286
DB 260 GCAGAACAGAAAGTTCAACTGCTTCGTAATTGGCATCAACTTCATG 305

RESULT 11

BM922638

LOCUS

DEFINITION AGENCOURT_6652776 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5755724.
5', mRNA sequence.

ACCESSION BM922638

VERSION 1

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 305)

NIH-MGC <http://www.ncbi.nlm.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapb3@nsl.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM12795 row: c column: 21

High quality sequence start: 52

High quality sequence stop: 628.

FEATURES

source

Location/Qualifiers

1..1152

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5755724"

/clone_lib="NIH_MGC_118"

/tissue_type="leukocyte"

/lab_host="DH10B"

/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV. (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb. Insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 354 a 273 c 276 g 249 t

ORIGIN

Query Match 60.7%; Score 264.2; DB 14; Length 1152;
Best Local Similarity 91.3%; Pred. No. 1.6e-51;
Matches 337; Conservative 0; Mismatches 23; Indels 9; Gaps 5;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 60
DB 470 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 529
QY 61 GAATCTCCAACTTAATCTTGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 120
DB 530 GAATCTCCAACTTAATCTTGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 589
QY 121 AAATATATCACACATATTGCTGGAGTCATGACATCAAGTTAAAGGCTTTGTCGA 180
DB 590 AAATATATCACACATATTGCTGGAGTCATGACATCAAGTTAAAGGCTTTGTCGA 649
QY 181 AAGATGCTGTCATGAGCCAAATAGATCAGATCAAGATCAAGTGTCCACACACA 240
DB 650 AAGATGCTGTCATGAGCCAAATAGATCAGATCAAGATCAAGTGTCCACACACA 709
QY 241 GCAG-AACAGAAAGTTCAACTGCTTCGTAATT-GGCATCAACTTCATGAGAA--GAAAG 295
DB 710 GCAGAAACAGAAAGTTCAACTGCTTCGTAATTGGGCATCAACTTCATGAGAAAGA 769
QY 296 AAGCGTATGACACATT-GATTAAAGATCTCAAAAAA---GCCAATCTTTGTACTTTGCA 351
DB 770 AAGCGTATGACACCTTGGATTAAAGATCTCAAAAAAGCCCAACCTTGGACCTCTGCG 829
QY 352 GAGAAATTT 360
DB 830 AAGAAATTT 838

RESULT 12

AV715411

LOCUS

DEFINITION AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5', mRNA sequence.

ACCESSION AV715411

VERSION AV715411.1

KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 696)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,

Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z. and Han, Z.
 Homo sapiens cDNA DCB clones
 Unpublished (2000)
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shouying Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P.R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

Location/Qualifiers

FEATURES

source

1. .696
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DCBAUC01"
 /clone_lib="DCB"
 /cell_type="dendritic cells"
 /dev_stage="mature"
 /lab_host="BM25.8"
 /note="Vector: pTriplex2; Site_1: sfIIA; Site_2: sfIIB"

BASE COUNT 210 a 141 c 156 g 189 t

Query Match 46.3%; Score 201.2; DB:10; Length 696;
 Best Local Similarity 98.5%; Pred. No. 7.3e-37;
 Matches 203; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60
 |||||
 Db 478 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 537
 |||||
 Qy 61 GAATCTCAACCTTAAATCCTGAACAGTGCATGCAATTAATTTATCTGATGTTGACTTGAGT 120
 |||||
 Db 538 GAATCTCAACCTTAAATCCTGAACAGTGCATGCAATTAATTTATCTGATGTTGACTTGAGT 597
 |||||
 Qy 121 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 180
 |||||
 Db 598 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 657
 |||||
 Qy 181 AAGAATGGTGTCATGAAGCCAAAT 206
 |||||
 Db 658 AAGAATGGTGTCATGAAGCCAACT 683

RESULT 13

AA852070
 LOCUS HGBBT116 Human Glioblastoma Cell Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 AA852070
 AA852070
 VERSION
 AA852070.1 GI:2939608
 KEYWORDS
 EST.
 SOURCE
 human.

ORGANISM

Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 217)
 Jia, H.L., Hu, S.N., Tu, C., Yuan, J.G. and Qiang, B.Q.
 DRT-PCR of Human Glioblastoma Cell Line BT-325 cDNAs
 Unpublished (1997)

JOURNAL

CONTACT: Boqin Qiang
 National Laboratory of Medical Molecular Biology, CAMS & PUMC
 Institute of Basic Medical Sciences, Peking Union Medical College &
 Chinese Academy of Medical Sciences
 5 Dong Dan San Tiao, Beijing 100005, P.R. China
 Tel: (010) 65296411
 Fax: 8610-5240529

Email: zh357@iname.com

Seq primer: M13 Reverse Primer.

FEATURES

source

1. .217
 /organism="Homo sapiens"

/db_xref="taxon:9606"
 /clone_lib="Human Glioblastoma Cell"
 /cell_type="Glioblastoma Cell"
 /cell_line="BT-325"
 /lab_host="E.coli DH5a"
 /note="Organ: Brain; Vector: PCR11, Invitrogen; Total RNA
 was isolated from human glioblastoma cell line BT325.
 Then Differential Display RT-PCR was conducted between
 normal and all-trans Retinoic Acid induced cell.
 Differentially expressed PCR products were cloned and
 sequenced."

BASE COUNT 86 a 34 c 48 g 49 t

ORIGIN

Query Match 45.1%; Score 196.4; DB:9; Length 217;
 Best Local Similarity 99.5%; Pred. No. 8.2e-36;
 Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60
 |||||
 Db 20 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 79
 |||||
 Qy 61 GAATCTCAACCTTAAATCCTGAACAGTGCATGCAATTAATTTATCTGATGTTGACTTGAGT 120
 |||||
 Db 80 GAATCTCAACCTTAAATCCTGAACAGTGCATGCAATTAATTTATCTGATGTTGACTTGAGT 139
 |||||
 Qy 121 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 180
 |||||
 Db 140 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 199
 |||||
 Qy 181 AAGAATGGTGTCATGAATGAA 198
 |||||
 Db 200 AAGAATGGTGTCATGAATGAA 217

RESULT 14

H02935
 LOCUS Y146B08.r1 Soares placenta NB2HP Homo sapiens cDNA clone
 DEFINITION
 IMAGE:151767.5 similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
);, mRNA sequence.

ACCESSION H02935

VERSION H02935.1 GI:865868

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 461)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlffing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
 R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washo-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1432

High quality sequence stops: 316

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1432 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 316.

FEATURES

source

1. .461

/organism="Homo sapiens"

/db_xref="GDB:563902"

/db_xref="taxon:9606"
/clone="IMAGE:151767"
/clone_lib="Soares placenta Rb2HP"
/sex="female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AAGTGAAGAATTCGGCGCGCAGGAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo.
2 others

BASE COUNT 145 a 76 c 96 g 142 t 2 others
ORIGIN
Query Match 39.5%; Score 172; DB 14; Length 461;
Best Local Similarity 100.0%; Pred. No. 4.4e-30;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 264 TCCTAATGGCATCAACTTCATGGAAGAAAGAGCGTATGACACATTGATTAAGATCT 323
Db 1 TCCTAATGGCATCAACTTCATGGAAGAAAGAGCGTATGACACATTGATTAAGATCT 60
QY 324 CAAAAGAGCCATCTTTGTACTCTTCGAGAGAAATTCAGACTATCATCTCAAGGACAT 383
Db 61 CAAAAGAGCCATCTTTGTACTCTTCGAGAGAAATTCAGACTATCATCTCAAGGACAT 120
QY 384 TACTAGTACTCAGAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGCTC 435
Db 121 TACTAGTACTCAGAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGCTC 172

RESULT 15
AL542093
LOCUS
DEFINITION AL542093 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE0091I06 5 prime
, mRNA sequence.
ACCESSION AL542093
VERSION AL542093.1 GI:12873796
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .932
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE0091I06"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
technologies. Contact : feng liang life technologies, a
division of invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 270 a 210 c 233 g 218 t 1 others

ORIGIN

Query Match 38.9%; Score 169.4; DB 9; Length 932;
Best Local Similarity 98.3%; Pred. No. 2e-29;
Matches 170; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGACAGAAAGCAACCAAGCTTCTCAT 60
Db 753 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGACAGAAAGCAACCAAGCTTCTCAT 812
QY 61 GAATCTCCCAACCTTAAATCCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
Db 813 GAATCTCCCAACCTTAAATCCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 872
QY 121 AAATATATCAACCACTATTGCTGGAGTCATGACACTAAGTCAAGCTTAAAGCCTT 173
Db 873 AAATATATCAACCACTATTGCTGGAGTCATGACACTAAGTCAAGCTTAAAGCCTT 925

Search completed: June 15, 2003, 21:11:49
Job time : 1428 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 21:13:09 ; Search time 1535 Seconds
(without alignments)
2749.125 Million cell updates/sec

Title: US-09-884-987-2_COPY_175_319
Perfect score: 750
Sequence: 1 GWLCLLLPIPLVWKRKE.....KANLCTLAETIILKDKIT 145

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame-p2n.model -DEV=xlpl
-Q=cg2_1/USPTO.spool/US09884987/runat_09062003_140300_13176/app_query.fasta_1.327
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LISP=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09884987 -CGEN_1_1_1319=runat_09062003_140300_13176 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	750	100.0	761	9	HSPASCD52	247994 H.sapiens F
2	750	100.0	899	9	HSPAS4DEL	270519 H.sapiens F
3	750	100.0	920	9	HSPAS34	X83490 H.sapiens m
4	750	100.0	1008	6	E05336	E05336 DNA encodin
5	750	100.0	1457	6	E35160	E35160 Method for
6	750	100.0	2534	6	A87646	A87646 Sequence 4
7	750	100.0	2534	6	AR163572	AR163572 Sequence
8	750	100.0	2534	6	AR173438	AR173438 Sequence
9	750	100.0	2534	6	E05110	E05110 CDNA encodi
10	750	100.0	2534	6	E09121	E09121 CDNA encodi
11	750	100.0	2534	9	HUMFASANT	M67454 Human Fas a
12	750	100.0	2551	6	AR143111	AR143111 Sequence
13	750	100.0	2551	9	HSAP01	X63717 H.sapiens m
14	750	100.0	2719	9	BC012479	BC012479 Homo sapi
15	750	100.0	8282	6	AX146813	AX146813 Sequence
16	750	100.0	8345	6	AX146814	AX146814 Sequence
17	743	99.1	3009	6	AX060340	AX060340 Sequence
18	743	99.1	3009	6	AX060342	AX060342 Sequence
19	726	96.8	1468	6	AX060336	AX060336 Sequence
20	681	90.8	983	9	HSPASAP0A	266556 H.sapiens F
21	670	89.3	1483	6	AX060538	AX060538 Sequence
22	663	88.4	836	9	HSPASCD53	247995 H.sapiens F
23	663	88.4	836	9	HSPAS46DL	270520 H.sapiens F
24	663	88.4	857	9	HSPAS346	X83491 H.sapiens m
25	663	88.4	945	9	HSPASCD51	247993 H.sapiens F
26	663	88.4	1104	9	HSPAS6	X83493 H.sapiens m
27	663	88.4	2471	6	I58632	I58632 Sequence 18
28	663	88.4	2471	6	I63530	I63530 Sequence 18
29	584	77.9	996	9	AB031420	AB031420 Macaca fa
30	584	77.9	1342	9	AF344850	AF344850 Macaca ne
31	577	76.9	1068	9	AF326208	AF326208 Macaca as
32	569	75.9	1361	9	AF344843	AF344843 Carcacebu
33	562	74.9	1367	9	AF344833	AF344833 Macaca mu
34	557.5	74.3	1077	9	AY007572	AY007572 Macaca mu
35	554.5	73.9	975	6	AX331556	AX331556 Sequence
36	554.5	73.9	975	6	AX336715	AX336715 Sequence
37	554.5	73.9	975	9	HSPAS47	X83492 H.sapiens m
38	533	71.1	1324	9	AF344835	AF344835 Aotus trl
39	531	70.8	1005	9	AF332357	AF332357 Macaca ar
40	479	63.9	1840	9	HSAPT9	X81342 H.sapiens A
41	479	63.9	1846	11	G75384	G75384 csnpfrsf6
42	479	63.9	2774	9	HSPASX9	X82286 H.sapiens F
43	479	63.9	187313	9	AL157394	AL157394 Human DNA
44	471	62.8	963	4	AB021299	AB021299 Oryctoleg
45	471	62.8	2003	4	AB021296	AB021296 Oryctoleg

ALIGNMENTS

RESULT 1

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HSFASCD52
LOCUS       H.sapiens FAS Del 2 mRNA.              761 bp      mRNA      linear      PRI 15-DEC-1997
DEFINITION   H.sapiens FAS Del 2 mRNA.
ACCESSION   247994
VERSION     247994.1
KEYWORDS    GI:728579
SOURCE      FAS gene.
ORGANISM    Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 761)
AUTHOR      Ruberti,G.
TITLE       Direct Submission
JOURNAL     Submitted (24-JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,
Immunology, viale C.Marx 43, Rome, Italy, I-00137
REFERENCE   2 (bases 1 to 761)
AUTHOR      Cascino,I., Flucci,G., Papoff,G. and Ruberti,G.
TITLE       Three functional soluble forms of the human apoptosis-inducing Fas
molecule are produced by alternative splicing
JOURNAL     J. Immunol. 154 (6), 2706-2713 (1995).
MEDLINE     95181785
PUBMED      7533181
COMMENT     On Mar 25, 1995 this sequence version replaced gi:695540.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /isolate="GF"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /clone="FAS DEL2"
                     /cell_type="PHA-activated PBMC"
     CDS             1..312
                     /standard_name="FAS/Apo 1"
                     /note="alternative splicing variant of FAS gene missing
                     exons 3 and 4. Exons 5 and 6 translated in a different
                     frame up to new stop codon at 310."
                     /codon_start=1
                     /evidence="experimental"
                     /product="FAS soluble protein"
                     /protein_id="CAA88032.1"
                     /db_xref="GI:695541"
                     /db_xref="SPTREMBL:Q14294"
                     /translation="MLGIWTLLPLVLTSLVARLSSKSVNAQVTDINSKGLERKVTVT
                     ETQNLEGLHHDQFCHKPPDVMNMESSRNAHSPATSAKRKDDPLTWGGFVFPPFCQF
                     H"
     exon            <1..30
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                     /number=1
                     /evidence="experimental"
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                     /number=3
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                     /number=4
                     /note="translated in a different frame in this variant up
                     to a new stop codon at 310."
                     /number=4
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                     /number=5
                     /note="translated in this variant."
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                     /evidence="experimental"
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                     /number=6
                     /note="Not translated in this variant."
                     /number=6
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                     /number=7
                     /evidence="experimental"
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/exon            430..>761
/standard_name="FAS/Apo 1"
/note="Not translated in this variant."
/number=9
/evidence="experimental"
/number=9
BASE COUNT    261 a 154 c 156 g 190 t
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Alignment Scores:
Pred. No.:      2,91e-71      Length:      761
Score:          750.00        Matches:    145
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    100.00%      Indels:        0
DB:              9            Gaps:          0
US-09-884-987-2_COPY_175_319 (1-145) x HSFASCD52 (1-761)
QY      1 GlyTrrLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
Db      276 GGGTGGCTTTGCTCTTCTTTTGGCAATTCACATAATTTGGTGAAGAGAAAGGAA 335
QY      21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db      336 GTACAGAAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCACC 395
QY      41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTrpIleThr 60
Db      396 TTAATCTCTGAAACAGTGCACATAAATTTATCTGATGTGACTTGAGTAAATATATACCC 455
QY      61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db      456 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCAAGAAATGGTGC 515
QY      81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
Db      516 AATGAAGCCAAATAGATGACATCAAGATGACATGTCACAGACACAGACAGAA 575
QY      101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTrpAspThrLeu 120
Db      576 GTTCAACTGCTTCGTAATTTGGCATCACTTCACTTCACTTCACTTCACTTCACTTCACT 635
QY      121 IleLysAspLeuLysLysAlaAsnLeuLysGlyThrLeuAlaGluLysIleGlnThrIle 140
Db      636 ATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGCAGAGAAATTCAGACTATCATC 695
QY      141 LeuLysAspIleThr 145
Db      696 CTCAGGACATTAAT 710
RESULT 2
HSFAS4DEL
LOCUS       H.sapiens FAS/Apo 1 mRNA for FAS soluble protein (clone FAS
DEFINITION   H.sapiens FAS/Apo 1 mRNA for FAS soluble protein (clone FAS
EXON4DEL).
ACCESSION   Z70519
VERSION     Z70519.1
KEYWORDS    GI:1418817
SOURCE      FAS soluble protein; FAS/Apo 1 gene.
ORGANISM    Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 899)
AUTHORS     Papoff,G., Cascino,I., Erano,A., Starace,G., Lynch,D.H. and
Ruberti,G.
TITLE       A N-terminal domain shared by Fas soluble variants prevents cell
death in vitro.
JOURNAL     J. Immunol. (1996) In press
REFERENCE   2 (bases 1 to 899)
AUTHORS     Ruberti,G.
TITLE       Direct Submission
JOURNAL     Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R.,

```

Immunology, viale C.Marx 43, Rome, Italy, I-00137

FEATURES

Source

Location/Qualifiers

1..899
 /organism="Homo sapiens"
 /isolate="LN"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="FAS Exo4Del"
 /cell_type="PHA-activated PBMC"
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 /standard_name="FAS/Apo 1"
 /note="Alternative splicing variant of FAS gene missing exon 4. Exons 5 and 6 translated in a different frame up to a new stop codon at 448."
 /codon_start=1
 /evidence=experimental
 /product="FAS soluble protein"
 /protein_id="CAA94430.1"
 /db_xref="GI:1418818"
 /db_xref="SPTREMBL:Q14292"
 /translation="MLGWTLLPLVLTSTVARLSKSVNAQVTDINSKGLERKTVTV
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 KRCUCDEGHVNMESSNAHSPATPSAKRKPDLTWGGVFVFFCOFH"
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 31..196
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 197..334
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 397..459
 /note="Translated in a different frame in this variant up to a new stop codon at 448."
 /number=6
 /evidence=experimental
 460..542
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 /evidence=experimental
 543..567
 /note="Not translated in this variant."
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 /note="Not translated in this variant."
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exon

exon

exon

exon

exon

exon

exon

exon

BASE COUNT

ORIGIN 307 a 179 c 197 g 216 t

Alignment Scores:

Pred. No.: 3,548-71 Length: 899
 Score: 750.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x HSFAS4DEL (1-899)

QY 1 GlyTtPLeuCysLeuLeuLeuLeuProLeuLeuValTrpValLysArgLysGlu 20

Db 144 GGGTGGCTTGTCTCTCTTTTGGCAATTCACATTAATTTGGTGAAGAAAGGAA 473

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40

Db 474 GTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCATGATCTCAACC 533

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
 Db 534 TTAATCTGAAACAGTGGCAATAATTAATCTGATGTTGACTTGAGTAATATATACACC 593
 QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
 Db 594 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGCGTTTGTTCGAAAGAATGGTGTC 653
 QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
 Db 654 AATGAAGCAAAATAGATGAGATCAAGATGACCAATGTCCAAGACACAGCAGACAGAA 713
 QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaLysAspThrLeu 120
 Db 714 GTTCAACTGCTTCGTAATTCGATCACTTCATGGAAGAAAGAGCGTATGACACATTG 773
 QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
 Db 774 ATTAAGATCTCAAAAAGCAATCTTTGTACTCTTCGAGAGAAAATTCAGACTATCATC 833
 QY 141 LeuLysAspIleThr 145
 Db 834 CTCAAGGACATTACT 848

RESULT 3

HSFAS34

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

gene

exon

BASE COUNT

312 a 180 c 186 g 242 t

HSFAS34

H.sapiens mRNA for Fas/Apo-1 (clone pCRTM11-Fasdelta(3,4)).

X83490

X83490.1

GI:971454

FAS gene.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Cheng, J., Zhou, T., Liu, C., Shapiro, J.P., Brauer, M.J., Kiefer, M.C., Barr, P.J. and Mountz, J.D.

Protection from Fas-mediated apoptosis by a soluble form of the Fas molecule

Science 263 (5154), 1759-1762 (1994)

94182136

7510905

2 (bases 1 to 920)

Cheng, J.

Direct Submission

Submitted (14-DEC-1994)

J. Cheng, University of Alabama at Birmingham, Division of Clinical Immunol. & Rheum., UAB Station, LHRB 473, Birmingham AL 35294-0007, USA

3 (bases 1 to 920)

Liu, C., Cheng, J. and Mountz, J.D.

Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation

Biochem. J. 310 (Pt 3), 957-963 (1995)

96013198

7575433

Related sequences: M67454 and X63717.

Location/Qualifiers

1..920

/organism="Homo sapiens"

/isolate="healthy individual"

/db_xref="taxon:9606"

/chromosome="10"

/map="10q24.1 or 10q23"

/clone="PCR TM 11-Fas delta(3,4)"

/cell_type="peripheral blood mononuclear cells"

391..637

/gene="Fas/Apo-1"

391..637

/gene="Fas/Apo-1"

/note="3 and 4"

312 a 180 c 186 g 242 t

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ORIGIN
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Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x HSPAS34 (1-920)
Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProleProleLeuValTrpValLysArgLysGlu 20
Db 301 GGGTGGCTTTGCTCTCTCTTTTCCCAATCCCAATGTTGGTGAAGAGAAGAA 360
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 361 GTACAGAAACATCGAAGAGCAGAGAAAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 420
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
Db 421 TTAATCCTGAAACAGTGGCAATAATTTATCTGATGTTGACTGAGTAATAATATATCACC 480
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 481 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTGTTCGAAAGAATGGTGTC 540
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
Db 541 AATGACCCAAATAGATGATGATCAAGATGACAATGTCCAAGACACAGACAGACAGAAA 600
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLysGlyLysGlyLysGluAlaTyAspThrLeu 120
Db 601 GTTCAACTGCTGTGATGTCATCACTTCATGGAAGAAGAAGCGGTATGACACATG 660
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Db 661 ATTAAGATCTCAAAAAGGCAATCTTTGTACTCTTCAGAGAAAATTCAGACTATCATC 720
Qy 141 LeuLysAspThrLeu 145
Db 721 CTCAGGACATTTACT 735

RESULT 4
E05336
LOCUS DNA encoding human Fas protein.
DEFINITION E05336
ACCESSION E05336
VERSION E05336.1 GI:2173525
KEYWORDS JP 1993219959-A/2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NEW DNA AND PROTEIN CODED THEREWITH
JOURNAL OSAKA BIO SCI RENKIUISHO
OS OSAKA BIO SCI RENKIUISHO
PN JP 1993219959-A/2
PD 31-AUG-1993
PF 14-FEB-1997 JP 1992028090
PI OSAKA-JUICH
PC C12N15/12,C07K13/00,C12P21/02;
CC strandedness: Double;
CC topology: Linear;
CC *source: cell_line-KT-3;
FH key
FH key Location/Qualifiers
FT CDS
FT 1..1008
/product='Fas protein'.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 343 a 205 c 217 g 243 t
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Alignment Scores:
Pred. No.: 4.06e-71 Length: 1008
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x E05336 (1-1008)
Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProleProleLeuValTrpValLysArgLysGlu 20
Db 523 GGGTGGCTTTGCTCTCTCTTTTCCCAATCCCAATGTTGGTGAAGAGAAGAA 582
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 583 GTACAGAAACATCGAAGAGCAGAGAAAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 642
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
Db 643 TTAATCCTGAAACAGTGGCAATAATTTATCTGATGTTGACTGAGTAATAATATATCACC 702
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 703 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTGTTCGAAAGAATGGTGTC 762
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
Db 763 AATGACCCAAATAGATGATGATCAAGATGACAATGTCCAAGACACAGACAGACAGAAA 822
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLysGlyLysGlyLysGluAlaTyAspThrLeu 120
Db 823 GTTCAACTGCTGTGATGTCATCACTTCATGGAAGAAGAAGCGGTATGACACATG 882
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Db 883 ATTAAGATCTCAAAAAGGCAATCTTTGTACTCTTCAGAGAAAATTCAGACTATCATC 942
Qy 141 LeuLysAspThrLeu 145
Db 943 CTCAGGACATTTACT 957

RESULT 5
E35160
LOCUS Method for inducing apoptosis.
DEFINITION E35160
ACCESSION E35160
VERSION E35160.1 GI:18624419
KEYWORDS JP 2000102389-A/7.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1457)
AUTHORS Hagiwara, H., Aotsuka, Y. and Miyahara, J.
TITLE Method for inducing apoptosis
JOURNAL Patent: JP 2000102389-A 7 11-APR-2000;
YOSHIHIDE HAGIWARA, HIDEAKI HAGIWARA
OS Artificial Sequence
PN JP 2000102389-A/7
PD 11-APR-2000
PF 29-SEP-1998 JP 1998291441
PI HIDEAKI HAGIWARA, YASUYUKI AOTSUKA, JUNICHI MIYAHARA
PC C12N15/09,A61K31/00,A61K48/00,C07K16/42,C07K19/00,C12N5/10, PC
C12N15/02//
PC (C12N5/10,C12R1:91),C12N15/00,C12N5/00,C12N15/00,(C12N5/00, PC

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CC C12RI:91)
FH Key Location/Qualifiers
FT CDS (7)..(1317).
FEATURES
source
Location/Qualifiers
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/db_xref="taxon:32644"
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Db 832 GGGTGGCTTTGCTCTCTCTTTTGGCAATCCCACTAATTTGGTGAAGAGAAAGAA 891
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 892 GTACAGAAACATCGAAGAGCAGACAGAAAGAAACCAAGGCTTCTCATGAATCTCCAA 951
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
Db 952 TTAATCCTGAACAGTGGCAATAATTTATCTGATCTTGACCTGAGTAATATATATAT 1011
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 1012 ACTATTCGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCAAAGAAATGGTGC 1071
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 1072 AATGAACCAAAATAGATGAGATCAAGATGACATGTCCTCAAGACAGCAGACAGAA 1131
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
Db 1132 GTTCAACTGCTCGTAATTTGGCATCACTTCAATGGAAGAAAGAAAGCGTATGACAC 1191
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
Db 1192 ATTAAGATCTCAAAAAGCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1251
Qy 141 LeuLysAspIleThr 145
Db 1252 CTCAGGACATTAAT 1266
RESULT 6
A87646
LOCUS A87646 2534 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 4 from Patent W09835692.
ACCESSION A87646
VERSION A87646.1 GI:6736281
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2534)
AUTHORS Screaton,G.R. and Xu,X.
TITLE MATERIALS AND METHODS RELATING TO THE PROTECTION OF USEFUL IMMUNE CELLS
JOURNAL Patent: WO 9835692-A 4 20-AUG-1998;
SCREATION GAVIN ROBERT (GB);/ISIS INNOVATION (GB)
FEATURES
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/organism="unidentified"
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ORIGIN
Alignment Scores:
Pred. No.: 1.21e-70 Length: 2534
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-884-987-2_COPY_175_319 (1-145) x A87646 (1-2534)
Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
Db 717 GGGTGGCTTTGCTCTCTCTTTTGGCAATCCCACTAATTTGGTGAAGAGAAAGAA 776
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 777 GTACAGAAACATCGAAGAGCAGACAGAAAGAAACCAAGGCTTCTCATGAATCTCCAA 836
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
Db 837 TTAATCCTGAACAGTGGCAATAATTTATCTGATCTTGACCTGAGTAATATATATAT 896
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 897 ACTATTCGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCAAAGAAATGGTGC 956
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 957 AATGAACCAAAATAGATGAGATCAAGATGACATGTCCTCAAGACAGCAGACAGAA 1016
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
Db 1017 GTTCAACTGCTCGTAATTTGGCATCACTTCAATGGAAGAAAGAAAGCGTATGACAC 1076
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
Db 1077 ATTAAGATCTCAAAAAGCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136
Qy 141 LeuLysAspIleThr 145
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RESULT 7
A87646
LOCUS A87646 2534 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270998.
ACCESSION A87646
VERSION A87646.1 GI:16234218
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2534)
AUTHORS Nagata,S., Itoh,N. and Yonehara,S.
TITLE DNA coding for human cell surface antigen
JOURNAL Patent: US 6270998-A 1 07-AUG-2001;
FEATURES
source
Location/Qualifiers
1..2534
/organism="unknown"
BASE COUNT 817 a 487 c 503 g 727 t
ORIGIN
Alignment Scores:
Pred. No.: 1.21e-70 Length: 2534
Score: 750.00 Matches: 145
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Qy	1	GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpVallysArgLysGlu	20				
Dd	717	GGGTGGCTTTGCTCTCTCTTTGCCNATCCACTAATCTGTTGGGTGACAGAGAAAGGAA	775				
Qy	21	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	40				
Dd	777	GTACAGAAACATGCAGAAAGCAGAGAAAGAAACCAAGTCTCATGAATCTCCAACC	836				
Qy	41	LeuAsnProGluThrValAlaIleAsnLeuSerAspValasLeuSerLysTyrIleThr	60				
Dd	837	TTAAATCCTGAAACAGCTGGCAATAAATTTATCTCATGTTGACTTGACTGAATAATATATCACC	896				
Qy	61	ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal	80				
Dd	897	ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCAAAGAAGTGGTGC	956				
Qy	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys	100				
Dd	957	AATGAAGCCAAATAGATGAGATCAAGTAATGACAATCTCCAAGACACAGCAGAACAGAAA	1016				
Qy	101	ValGlnLeuLeuArgAsnThrHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu	120				
Dd	1017	GTTCAACTGCTTCGTAATTGGCATCAACTTCATGGAAAGAAGAAGCGTATGACACATTG	1076				
Qy	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140				
Dd	1077	ATTAAAGATCTCAAAAAGCAACTTTTGACTCTTCGAGAGAAATTCAGACTATCATC	1136				
Qy	141	LeuLysAspIleThr	145				
Dd	1137	CTCAGGACATTA	1151				
<p>RESULT 11</p> <p>HUMFASANT</p> <p>LOCUS</p> <p>DEFINITION</p> <p>ACCESSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p>							
<p>Human Fas antigen (fas) mRNA, complete cds.</p> <p>M67454.1 GI:182409</p> <p>Human sapiens (clone pf58) (tissue library: pCEV4) cDNA to mRNA.</p> <p>Human sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.</p> <p>1 (bases 1 to 2534):</p> <p>Itoh, N., Yonehara, S., Ishii, A., Yonehara, M., Mizushima, S., Samehima, M., Hase, A., Seto, Y. and Nagata, S.</p> <p>The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis</p> <p>Cell 66 (2), 233-243 (1991)</p> <p>91309137</p>							
<p>REFERENCE</p> <p>AUTHORS</p> <p>TITLE</p> <p>JOURNAL</p> <p>MEDLINE</p>							

QY	41	LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr	60
Db	863	TTAAATCTCGTGAACAGTGGCAATAAATTTATCTGATGTTGACTTCAGTAAATATATCACC	922
QY	61	ThrIleAlaGlyValIleMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal	80
Db	923	ACTATTGCTGGAGTGCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCGAAAGAAATGGTGTC	982
QY	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys	100
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QY	101	ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaIleThrLeu	120
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QY	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140
Db	1103	ATTAAAGATCTCAAAAGGCCAATCTTTGTACTCTTGCAGAGAAAATTCAGACTATCATC	1162
QY	141	LeuLysAspIleThr	145
Db	1163	CTCAGGACATTACT	1177
RESULT 14			
LOCUS	BC012479		
DEFINITION	Homo sapiens, Similar to tumor necrosis factor receptor superfamily, member 6, clone MGC:21432 IMAGE:4514272, mRNA, complete cds.	2719 bp	mRNA linear PRI 20-AUG-2001
ACCESSION	BC012479		
VERSION	BC012479		
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2719)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submission		
REMARK	Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalob@bcm.tmc.edu Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 28 Row: 1 Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein. Location/Qualifiers 1. .2719 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:21432 IMAGE:4514272" /tissue_type="Bladder, transitional cell papilloma" /clone_lib="NIH_MGC_93" /lab_host="DH10B"		
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DB	863	TTAAATCTCGTGAACAGTGGCAATAAATTTATCTGATGTTGACTTCAGTAAATATATCACC	922
QY	61	ThrIleAlaGlyValIleMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal	80
DB	923	ACTATTGCTGGAGTATGACACAAAGTCAAGTAAAGGCTTTGTTTTCGAAAGAAATGGTGC	982
QY	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys	100
DB	983	AATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAGACACAGCAGACAGAA	1042
QY	101	ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaIleThrLeu	120
DB	1043	GTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGTAAGAAAGAACGCTATGACACATG	1102
QY	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140
DB	1103	ATTAAGATCTCAAAAGGCCAATCTTTGTACTCTTGCCAGAGAAAATTCAGACTATCATC	1162
QY	141	LeuLysAspIleThr	145
DB	1163	CTCAGGACATTTACT	1177
RESULT 14			
LOCUS	BC012479		
DEFINITION	Homo sapiens, Similar to tumor necrosis factor receptor superfamily, member 6, clone MGC:21432 IMAGE:4514272, mRNA, complete cds.	2719 bp	mRNA linear PRI 20-AUG-2001
ACCESSION	BC012479		
VERSION	BC012479.1	GI:15214691	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2719)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submission		
REMARK	Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalob@bcm.tmc.edu Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 28 Row: 1 Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein. Location/Qualifiers 1. .2719 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:21432 IMAGE:4514272" /tissue_type="Bladder, transitional cell papilloma" /clone_lib="NIH_MGC_93" /lab_host="DH10B"		
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JOURNAL Patent: WO 0134806-A 7 17-MAY-2001;
Rigel Pharmaceuticals, Inc. (US)
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Score: 750.00 Matches: 145
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Db 4221 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCAAGAAATGGTGTTC 4162
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QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
Db 4101 GTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAAAGCGTATGACACATG 4042
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Db 4041 ATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTGCAGAGAAAATTCAGACTATCATC 3982
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Search completed: June 15, 2003, 22:33:17
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BASE COUNT 904 a 532 c 531 g 752 t
ORIGIN
Alignment Scores:
Pred. No.: 1.31e-70 Length: 2719
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 1 GlyTrpLeuCysLeuLeuLeuProLeuLeuValTrpValLysArgLysGlu 20
Db 833 GGGTGGCTTTGCTCTCTTTGGCAATTCACATAATTTGTTGGTGAAGAGAAAGGAA 892
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 893 GTACAGAAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCAACC 952
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrLeuThr 60
Db 953 TTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACC 1012
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 1013 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCAAGAAATGGTGTTC 1072
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 1073 AATGAAGCCAAATAGATGAGATCAAGATGACATGTCCAAGACACACAGACAGAA 1132
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
Db 1133 GTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAAAGCGTATGACACATG 1192
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Db 1193 ATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTGCAGAGAAAATTCAGACTATCATC 1252
QY 141 LeuLysAspIleThr 145
Db 1253 CTCAGGACATTACT 1267
RESULT 15
AX146813/c
LOCUS AX146813 8282 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 7 from Patent WO0134806.
ACCESSION AX146813
VERSION AX146813.1 GI:14285162
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 8282)
AUTHORS Kinseila,T.M.
TITLE Methods and compositions for screening using diphtheria toxin constructs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 21:11:59 ; Search time 217 Seconds
(without alignments)
1504.792 Million cell updates/sec

Title: US-09-884-987-2_COPY_175_319

Perfect score: 750

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4310478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 17: /SID2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	750	100.0	920	17	AAT34529	Human Fas soluble
2	750	100.0	920	24	ABK84693	Human cDNA differe
3	750	100.0	1167	17	AAT34526	Human Fas antigen
4	750	100.0	1457	21	AAA39167	Apocobody3sc fusi
5	750	100.0	2534	13	AAQ29959	Human cell surface
6	750	100.0	2534	16	AAQ95297	Plasmod pf58 contg
7	750	100.0	2534	17	AAT16303	hFas coding sequen
8	750	100.0	2534	18	AAV07002	Human Fas antigen
9	750	100.0	2534	19	AAV32993	Fas cDNA. Mammali
10	750	100.0	2551	21	AAAC61798	DNA encoding a hum
11	750	100.0	2551	24	ABN79588	Human Fas locus HS
12	750	100.0	8282	21	AAZ34938	C12ScFas survival
13	750	100.0	8282	22	AAF30947	C12ScFas survival
14	750	100.0	8345	21	AAZ34939	Abhhh survival con
15	750	100.0	8345	22	AAF30948	Abhhh survival con
16	743	99.1	3009	22	AAA91131	Fit-lextraFas/cy
17	743	99.1	3009	22	AAA91132	Flk-lextraFas/cy
18	726	96.8	1468	22	AAA91129	CD44hextraFas/cy
19	670	89.3	1483	22	AAA91130	CD44hextra/cmfascy
20	663	88.4	836	24	ABN79685	Sequence #9 used t
21	663	88.4	1104	17	AAT34527	Human Fas soluble
22	663	88.4	2471	16	AAQ93879	Fas-delta-TM cDNA.
23	663	88.4	2471	20	AAQ24878	Soluble Fas recept
24	658	87.7	857	17	AAT34530	Human Fas soluble
25	601	80.1	398	24	ABL79512	Human ovarian canc
26	566	75.5	460	24	ABL80178	Human Fas soluble
27	554.5	73.9	975	17	AAT34528	Breast cancer rela
28	554.5	73.9	975	24	ABL63728	Kidney cancer rela
29	554.5	73.9	975	24	ABN68887	Sequence #8 used t
30	465	62.0	1840	24	ABN79684	Murine Fas gene.
31	314.5	41.9	984	14	AAQ48008	DNA encoding a mur
32	314.5	41.9	1480	21	AAAC61859	Mouse fas locus MU
33	314.5	41.9	1480	24	ABN79649	Murine Fas antigen
34	314.5	41.9	1506	16	AAQ95302	Coding sequence fo
35	314.5	41.9	1506	17	AAT16305	Fas ligand (FasL)
36	314.5	41.9	1506	20	AAV71961	Sequence #6 used t
37	153	20.4	338	24	ABN79682	Human Fas antigen
38	111	14.8	80	21	AAA39161	Human spliced tran
39	101	13.5	60	24	ABN40425	Human spliced tran
40	101	13.5	60	24	ABN58760	Human spliced tran
41	101	13.5	60	24	ABN58963	Fas antigen antise
42	99.5	13.3	257	17	AAT34538	Human spliced tran
43	93	12.4	60	24	ABN58759	Sequence #5 used t
44	89	11.9	855	24	ABN79681	Chemically treated
45	86	11.5	15923	24	ABL70179	

ALIGNMENTS

RESULT 1

AAT34529

ID AAT34529 standard; cDNA; 920 BP.

XX

AC AAT34529;

XX 10-OCT-1996 (first entry)

XX

DE Human Fas soluble antigen Fas del3 cDNA.

XX

XX Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;

KW angioimmunoblastic lymphadenopathy; AILD; SS.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

FT 26..307 /*tag= a

PT DNA encoding human cell surface antigen - used to clarify
 PT apoptosis mechanism of various types of cell, and to prepare
 PT monoclonal antibodies that react with tumour cells expressing Fas

PS Claim 3; Fig 1 and 2; 27pp; English.

XX A cDNA library was prepared from polyA+ RNA from the human lymphoma
 CC cell line KT-3. The cDNA was ligated to BstXI-cut vector pCEV4 via
 CC BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-
 CC 7 cells which were then suspended in buffer containing murine anti-Fas
 CC Ab. The cells were "panned" on plates pre-coated with goat anti-mouse
 CC antibodies. The Fas-expressing cells adhered to the plates.
 CC Extrachromosomal DNA was prepared from adhered cells and used to
 CC transform E. coli VM100 cells. A 520bp XhoI-BamHI fragment from a
 CC positive clone (pF3) was used to screen the KT-3 cDNA library. The
 CC longest cDNA clone was designated pF58 and contains an ORF corresp.
 CC to a 335 amino acid pre-protein and a 319 amino acid mature protein
 CC (i.e. human Fas antigen).

XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Alignment Scores:

Pred. No.: 8,9e-83 Length: 2534
 Score: 750.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAQ29597 (1-2534)

QY 1 GlyTrpLeuLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
 DB 717 GGGTGGCTTGTCTCTCTTTTCCCAATCCACTTAATTTGGGTGAAGAGAAAGAA 776
 QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
 DB 777 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCCCAACC 836
 QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
 DB 837 TTAATTCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACCTGAGTAAATATATCACC 896
 QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
 DB 897 ACTATTGCTGGAGTCATGACACATGACATGACATGACATGACATGACATGACATG 956
 QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
 DB 957 AATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1016
 QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
 DB 1017 GTTCAACTGCTTCTGTAATTTGGCATCACTTCACTGGAAGAAAGAGCGTATGACATTC 1076
 QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
 DB 1077 ATTAAGATCTCAAAAGCCCAATCTTTGTACTCTTTCAGAGAAATTCAGACTATCATC 1136
 QY 141 LeuLysAspIleThr 145
 DB 1137 CTCAAGGACATTACT 1151

RESULT 6

AAQ95297
 ID AAQ95297 standard; cDNA; 2534 BP.

XX AC AAQ95297;
 XX DT 19-FEB-1996 (first entry)
 XX DE Plasmid pF58 contg. human Fas cDNA.
 XX

KW Plasmid pF58; human Fas cDNA; soluble membrane protein;
 KW antibody production; diseases; treatment; prevention; ds.
 XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 195..1202

XX FT /*tag= a

XX FT sig_peptide 195..242

XX FT /*tag= b

XX FT mat_peptide 243..1199

XX FT /*tag= c

XX JF07115988-A.

XX 09-MAY-1995.

XX 26-OCT-1993; 93JP-0267644.

XX 26-OCT-1993; 93JP-0267644.

XX (NIBS) JAPAN TOBACCO INC.

XX WPI; 1995-202847/27.

XX P-PSDB; AAR78606.

XX Preparation of soluble membrane proteins - for their use in antibody
 PT production for the treatment and prevention of related diseases
 XX Example 1; Pages 15-17; 51pp; Japanese.

XX AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The
 CC plasmid was used in the construction of an expression vector for
 CC the prodn. of recombinant soluble membrane proteins. The proteins
 CC can be used in antibody prodn. for the treatment and prevention of
 CC related diseases.

XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Alignment Scores:

Pred. No.: 8,9e-83 Length: 2534
 Score: 750.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAQ95297 (1-2534)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
 DB 717 GGGTGGCTTGTCTCTCTTTTCCCAATCCACTTAATTTGGGTGAAGAGAAAGAA 776
 QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
 DB 777 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCCCAACC 836
 QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
 DB 837 TTAATTCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACCTGAGTAAATATATCACC 896
 QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
 DB 897 ACTATTGCTGGAGTCATGACACATGACATGACATGACATGACATGACATGACATG 956
 QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
 DB 957 AATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1016
 QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
 DB 1017 GTTCAACTGCTTCTGTAATTTGGCATCACTTCACTGGAAGAAAGAGCGTATGACATTC 1076

QY 121 IleLysAspLeuLysAlaAsnLeuLysCysThrLeuAlaGluLysIleGlnThrIle140
 DB 1077 ATTAAGATCTCAAAAGCCCAATCTTGCTACTCTTGCGAGAAATTCAGACTATCATC 1136

QY 141 LeuLysAspIleThr 145
 DB 1137 CTCAAGGACATTACT 1151

RESULT 7
 AAT16303
 ID AAT16303 standard; cDNA; 2534 BP.
 AC AAT16303;
 XX 06-SEP-1996 (first entry)
 DT hFas coding sequence from plasmid pCEV4/hFas.
 DE hFas: antigen; immunosay; monoclonal antibody; autoimmune disease; SLE;
 KW rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
 XX Synthetic.

XX Key Location/Qualifiers
 FH 195..1201
 CDS /tag- a
 FT /product- Fas antigen
 FT sig_peptide 195..242
 FT /tag- b
 FT mat_peptide 243..1998
 FT /tag- c
 XX WO9601277-A1.
 PN 18-JAN-1996.
 PD 03-MAR-1995; 95WO-JP00349.
 PF 14-FEB-1995; 95JP-0025637.
 PR 06-JUL-1994; 94JP-0154706.
 XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
 PA (NISB) JAPAN TOBACCO INC.
 XX Hachiya T, Noguchi J, Yonehara S;
 XX WPI; 1996-087635/09.
 DR P-PSDB; AAR92528.
 XX Immunosay method for soluble Fas antigen in body fluids - for
 PT diagnosis of autoimmune diseases such as rheumatoid arthritis and
 PT systemic lupus erythematosus
 XX Example 8; Page 49-52; 124pp; Japanese.
 PS This sequence represents the coding sequence for the human Fas antigen
 CC contained within the plasmid pCEV4/hFas. The soluble Fas antigen is
 CC included in the Immunosay kit of the invention. The kit is for the
 CC assay of soluble Fas antigen and contains an immobilised anti-soluble Fas
 CC monoclonal antibody, as well as the standard soluble Fas antigen encoded
 CC by this sequence. The assay is simple and has high accuracy, high
 CC sensitivity, and is capable of assaying a number of different specimens
 CC at the same time. The Immunosay is used on biological samples (such as
 CC serum) and is useful for diagnosis of autoimmune diseases such as
 CC rheumatoid arthritis or systemic lupus erythematosus (SLE).
 XX Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;

Alignment Scores:
 Pred. No.: 8.9e-83 Length: 2534
 Score: 750.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAT16303 (1-2534)

QY 1 GlyTrpLeuLysLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
 DB 717 GCGTGGCTTTGCTCTCTCTTTGCAATTCACATAATTTGGTGGTGAAGAAAGGAA 776

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
 DB 777 GTACAGAAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCATGAATCTCAACC 836

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysIleThr 60
 DB 837 TTAATATCTCTGAACACAGTGGCAATAATTTATCTGATTTGACTTGAGTAAATATATCACC 896

QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
 DB 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGAAAGAAATGGTGTG 956

QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
 DB 957 AATGAAGCCAAATAGATGAGATCAAGATGACATGTCCAAGACACACAGACAGAGAAA 1016

QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaIleValTrpVal 120
 DB 1017 GTTCAACTGCTTCGTAATTTGGCATCAACTCATGTAAGAAAGAAAGGCGTATGACACATTG 1076

QY 121 IleLysAspLeuLysAlaAsnLeuLysCysThrLeuAlaGluLysIleGlnThrIleIle 140
 DB 1077 ATTAAGATCTCAAAAGCCCAATCTTTGCTACTCTTGCGAGAAATTCAGACTATCATC 1136

QY 141 LeuLysAspIleThr 145
 DB 1137 CTCAAGGACATTACT 1151

RESULT 8
 AAV07002
 ID AAV07002 standard; cDNA to mRNA; 2534 BP.
 XX AAV07002;
 AC 16-JUL-1998 (first entry)
 DT Human Fas antigen cDNA.
 XX Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
 KW apoptosis modulation; ss.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH 195..1202
 CDS /tag- a
 FT sig_peptide 195..242
 FT /tag- b
 FT mat_peptide 243..1199
 FT /tag- c
 FT /product- Fas_antigen
 XX WO9742319-A1.
 PN 13-NOV-1997.
 PD 01-MAY-1997; 97WO-JP01502.
 PF 02-MAY-1996; 96JP-0135760.
 PR (MOCH) MOCHIDA PHARM CO LTD.
 XX (OSAB-) OSAKA BIOSCIENCE INST.

PI Nagata S, Nakamura N;
 XX WPI; 1997-558981/51.
 DR P-PSDB; AAW50289.
 XX
 PT Fas antigen derivative containing modified extracellular region -
 PT has low antigenicity, promotes apoptosis and is useful in treatment
 PT of viral and other diseases
 XX
 PS Disclosure; Fig 1-2; 102pp; Japanese.
 XX
 CC The present sequence was used in the development of novel Fas
 CC antigen derivatives, which contain a Fas antigen extracellular
 CC region lacking one or more amino acid residues in the region from
 CC the amino-terminal to (but excluding) the 1st cysteine residue
 CC (preferably at least 29 residues are deleted).
 CC The derivatives are effective regulators of apoptosis and can be
 CC used (either by administration of the polypeptide, or by the use
 CC of the coding DNA in gene therapy) to treat a range of diseases,
 CC e.g. diabetes, arthritis, lupus and in particular viral diseases
 CC such as hepatitis, influenza and HIV, by modulating apoptosis of
 CC virus-infected cells.
 XX
 SQ Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;

Alignment Scores:
 Pred. No.: 8.9e-83 Length: 2534
 Score: 750.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAV07002 (1-2534)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
 Db 717 GGGTGGCTTGTCTTCTTCTTTTGGCAATTCCTAATTTGGGTGAAGAGAAAGAA 776
 QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
 Db 777 GTACAGAAACATGTCGAAAGACAGACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 836
 QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
 Db 837 TTAATCCTGAACAGCTGGCAATTAATTTATCTGTGACTGTGAGTAATATATACACC 896
 QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
 Db 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTCTTCAAGAAAGATGGTGTC 956
 QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
 Db 957 AATGAAGCCAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1016
 QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrAspThrLeu 120
 Db 1017 GTTCACTGCTGCTAATTTGGCATCACTTCATGGAAGAAAGACGCGTATGACATG 1076
 QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
 Db 1077 ATTAAGATCTCAAAAAGCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136
 QY 141 LeuLysAspIleThr: 145
 Db 1137 CTCAGGACATTACT 1151

RESULT 9
 AAV32993
 ID AAV32993 standard; cDNA; 2534 BP.
 XX
 AC AAV32993;
 XX

DT 18-NOV-1998 (first entry)
 XX Fas cDNA.
 DE
 XX
 KW Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
 KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
 KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
 KW prophylactic; AIDS; ss.
 XX
 OS Mammalia sp.
 XX
 FH Key Location/Qualifiers
 DE CDS 195..1202
 FT /*tag= a
 FT /product= "Fas protein"
 FT sig_peptide 195..242
 FT /*tag= b
 FT mat_peptide 243..1199
 FT /*tag= c
 FT polyA_signal 1831..1836
 FT /*tag= d
 XX
 PN WO9835692-A1.
 XX
 XX 20-AUG-1998.
 XX
 XX 17-FEB-1998; 98WO-GB00485.
 XX
 PR 17-FEB-1997; 97GB-0003276.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 XX
 XX Scream GR, Xu X;
 XX
 DR WPI; 1998-456867/39.
 DR P-PSDB; AAW49104.
 XX
 PT Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
 PT diseases - by interfering with interaction of Fas with Fas-ligand
 PT expressed on activated CD4+ cells, e.g. cells infected with HIV
 XX
 XX Disclosure; Fig 10; 71pp; English.
 XX
 CC The present sequence represents a Fas cDNA sequence used in the
 CC method of the invention. The method is concerned with reducing
 CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
 CC cells in an immune cell population which also comprises of Fas-ligand
 CC (FasL)-expressing activated CD4+ cells. It involves contacting this
 CC immune cell population with an effective amount of an agent (e.g. a
 CC soluble Fas-Fc fusion protein) which would interfere with the
 CC interaction between Fas and FasL. Therefore, the method is useful for
 CC identifying suitable agents which can reduce depletion of activated
 CC Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
 CC is the use of the agent in the manufacture of therapeutic compositions.
 CC Apoptosis of lymphocytes can be triggered by the interaction of the
 CC cell surface receptor Fas and its ligand FasL. By interfering with
 CC this interaction, the method described and its preparations can prevent
 CC apoptosis of CD8+ TK lymphocytes caused by expression of FasL on
 CC activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
 CC especially the result of CD4+ cell infection with an immunodeficiency
 CC virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
 CC virus (SIV). The claimed prevention of apoptosis may then allow
 CC maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
 CC towards the CD4+ cells infected with the infectious agent, enabling
 CC treatment (prophylactic and/or therapeutic) of immunodeficiency
 CC diseases e.g. AIDS.
 XX
 SQ Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Alignment Scores:
 Pred. No.: 8.9e-83 Length: 2534
 Score: 750.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAV32993 (1-2534)

QY 1 GlyTTPLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
DB 717 GGGTGGCTTGTCTCTCTCTTTGGCAATTCACATTAATGTTGGTGAAGAGAAAGGAA 776
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 777 GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 836
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThr 60
DB 837 TTAATCTGTAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATATCACC 896
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGAAGAAATGGTGTCT 956
QY 81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 957 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAGACACAGACAGAA 1016
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyraSpThrLeu 120
DB 1017 GTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCGTATCAGACATG 1076
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 1077 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136
QY 141 LeuLysAspIleThr 145
DB 1137 CTCAGGACATTACT 1151

RESULT 10

AC61798
ID AAC61798 standard; DNA; 2551 BP.

XX
AC AAC61798;

DT 06-MAR-2001 (first entry)

DE DNA encoding a human Fas (Apo-1) protein.

KW Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;
KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
KW autoimmune disease; inflammatory disease; lymphoma; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 221..1228

FT /tag- a "Fas"
FT /product- "Fas"

XX WO200061150-A1.
XX
XX
XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-US09540.

XX 12-APR-1999; 99US-0290640.

XX (ISIS-) ISIS PHARM INC.

XX Dean NM, Marcusson EG;

XX WPI; 2000-628395/60.

DR P-PSDB; AAB19341.

XX

PT Antisense oligonucleotides for treating hepatitis and colon, liver or
PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
PT 1 (Fap-1) expression

XX

PS Example 2; Page 71-73; 116pp; English.

XX

CC The present sequence encodes human Fas (Apo-1). The specification
CC describes antisense compounds which are targeted to the 5'-untranslated
CC region, translational start site, translational termination region
CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
CC ligand (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine
CC phosphatase). The antisense compounds are used to inhibit the
CC expression of Fas, FasL or Fap-1 in cells or tissues. They are used
CC to treat autoimmune or inflammatory diseases such as hepatitis. They
CC can also be used to treat cancer, especially colon, liver or lung
CC cancer or lymphoma.

XX

SQ Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;

Alignment Scores:

Pred. No.: 8,99e-83 Length: 2551
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAC61798 (1-2551)

QY

1 GlyTTPLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
DB 743 GGGTGGCTTGTCTCTCTCTTTGGCAATTCACATTAATGTTGGTGAAGAGAAAGGAA 802

QY

21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 803 GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 862

QY

41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
DB 863 TTAATCTGTAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATATCACC 922

QY

61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 923 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGAAGAAATGGTGTCT 982

QY

81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 983 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAGACACAGACAGAA 1042

QY

101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyraSpThrLeu 120
DB 1043 GTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCGTATCAGACATG 1102

QY

121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 1103 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1162

QY

141 LeuLysAspIleThr 145

DB 1163 CTCAGGACATTACT 1177

RESULT 11

ABN79588

ID ABN79588 standard; DNA; 2551 BP.

XX

AC ABN79588;

XX

DT 29-JUL-2002 (first entry)

XX

DE Human Fas locus HSAPO1.

XX

KW Human; immunosuppressive; antiinflammatory; hepatotropic;

CC then induced with IL-4 or IL-13, and the presence or absence of the
CC reporter gene is detected. Absence of the reporter gene indicates
CC that the agent inhibits the promoter.

XX
SQ Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;

Alignment Scores:
Pred. No.: 4.63e-82 Length: 8282
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAZ34938 (1-8282)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProileProleuLeuValTrpValLysArgLysGlu 20
DB 4401 GGTTGGCTTTGCTCTCTCTTTTCCCAATTCACATAATTTGGGTGAAGAGAAAGAA 4342
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 4341 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGATCTCCAAAC 4282
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
DB 4281 TTAATCTGAAACAGTGGCAATAATTTATCTGATCTTGACCTGAGTAAATATATACAC 4222
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 4221 ACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCAAGAGATGGTGT 4162
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 4161 ATGAAGCCAAATAGATGAGATCAAGATGACATGTCCAGACAGACAGACAGAA 4102
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
DB 4101 GTTCAACTGCTTGTAAATTTGGCATCACTTTCATGAAAGAAAGAGCGTATGACACATTG 4042
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 4041 ATTAAGATCTCAAAAGCAATCTTTGTACTCTTCGACAGAAATTCAGACTATCATC 3982
QY 141 LeuLysAspIleThr 145
DB 3981 CTCAAGGACATTACT 3967

RESULT 13

ID AAF30947/C

XX AAF30947 standard; DNA; 8282 BP.

XX AC AAF30947;

XX 23-JUL-2001 (first entry)

XX C12ScFas survival construct.

XX Interleukin-4 inducible epsilon promoter; human; IgE; antibody;

KW immunoglobulin E; allergy; therapy; switch rearrangement; vector;

KW Fas; survival construct; death gene; ds.

XX Chimeric - Unidentified.

XX W0200134806-A2.

XX 17-MAY-2001.

XX 13-NOV-2000; 2000WO-US31232.

XX 12-NOV-1999; 99US-0165189.

XX (RIGE-) RIGEL PHARM INC.

XX Kinsella TM;
PI WPI; 2001-335931/35.
DR
XX

PT Screening for agents capable of inhibiting a promoter, especially
PT interleukin-4 inducible epsilon promoter involved in immunoglobulin E
PT production, by using diphtheria toxin constructs -

XX Disclosure; Fig 12A-C; 80pp; English.

CC The present sequence is that of survival construct C12ScFas in
CC which the interleukin-4 inducible epsilon promoter-chimeric
CC Fas(CD95)-internal ribosome entry site-hygromycin-bovine growth
CC hormone polyA tail is placed in the C12s vector backwards so that
CC no leaky transcription occurs through the CMV promoter. Methods of
CC the invention utilize diphtheria toxin for screening purposes,
CC especially for identifying modulators of IgE synthesis, secretion
CC and switch rearrangement. A claimed method of screening for
CC bioactive agents capable of inhibiting the IL-4 inducible epsilon
CC promoter (see AAF30941), which is involved in IgE switching,
CC comprises: combining a candidate bioactive agent and a cell that
CC does not endogenously express heparin-binding epidermal growth
CC factor-like growth factor (HBEGF) and which comprises a fusion
CC nucleic acid encoding HBEGF; inducing the promoter with IL-4;
CC adding diphtheria toxin to the cell; and determining whether the
CC cell is dead. Survival constructs carrying a death gene and a
CC drug selectable marker have been used to generate an epsilon
CC promoter survival cell line. Inhibitors of IgE synthesis can be
CC identified that prevent the production of IgE and reduce or
CC eliminate an allergic response.

XX SQ Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;

Alignment Scores:

Pred. No.: 4.63e-82 Length: 8282
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAF30947 (1-8282)

QY 1 GlyTrpLeuCysLeuLeuLeuProileProleuLeuValTrpValLysArgLysGlu 20
DB 4401 GGTTGGCTTTGCTCTCTCTTTTCCCAATTCACATAATTTGGGTGAAGAGAAAGAA 4342
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 4341 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGATCTCCAAAC 4282
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
DB 4281 TTAATCTGAAACAGTGGCAATAATTTATCTGATCTTGACCTGAGTAAATATATACAC 4222
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 4221 ACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCAAGAGATGGTGT 4162
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 4161 ATGAAGCCAAATAGATGAGATCAAGATGACATGTCCAGACAGACAGACAGAA 4102
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
DB 4101 GTTCAACTGCTTGTAAATTTGGCATCACTTTCATGAAAGAAAGAGCGTATGACACATTG 4042
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 4041 ATTAAGATCTCAAAAGCAATCTTTGTACTCTTCGACAGAAATTCAGACTATCATC 3982

QY 141 LeuLysAspIleThr 145
 DB 3981 CTCAGGACATTAAT 3967
 RESULT 14
 AA234939/c
 ID AA234939 standard; DNA; 8345 BP.
 AC AA234939;
 XX 28-FEB-2000 (first entry)
 DT
 XX Ahhhh survival construct.
 XX Interleukin-4 inducible epsilon promoter; immunoglobulin;
 KW Ige; antibody; modulator; screening; human; allergy; therapy;
 KW reporter; survival construct; ds.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Bos taurus.
 OS Chimeric - Unidentified.
 XX WO958663-A1.
 PN 18-NOV-1999.
 PD 12-MAY-1999; 99WO-US10497.
 PF 12-MAY-1998; 98US-0076624.
 PR (RIGE-) RIGEL PHARM INC.
 XX
 XX Ferrick DA, Swift SE, Armstrong R, Fox B;
 PI WPI; 2000-062297/05.
 DR Methods, cell lines and vectors for screening for modulators of
 PT immunoglobulin E synthesis, secretion and switch rearrangement
 XX
 PS Disclosure; Fig 13A-C; 81pp; English.
 CC This is the nucleotide sequence of Ahhhh survival construct
 CC comprising an inducible epsilon promoter-chimeric Fas (either CD8
 CC or mlyt2)-IRES-hydromycin-bovine growth hormone poly-A tail placed
 CC in vector Cl2s backwards so that no leaky transcription occurs
 CC through the CMV promoter. It is an example of a death gene that
 CC provides a nucleic acid that encodes a protein which causes a
 CC cell to die. The death gene can be used as a reporter gene in
 CC methods of the invention used to screen for modulators of Ige
 CC synthesis, secretion and switch rearrangement. The method
 CC comprises combining a candidate bioactive agent, optionally linked
 CC to a fusion partner, with a cell comprising a fusion nucleic acid
 CC composed of the IL-4 inducible epsilon promoter (see AA234932), and
 CC a reporter gene, such as the present death gene. The promoter is
 CC then induced with IL-4 or IL-13, and the presence or absence of the
 CC reporter gene is detected. Absence of the reporter gene indicates
 CC that the agent inhibits the promoter.
 XX
 SQ Sequence 8345 BP; 1915 A; 2264 C; 2084 G; 2082 T; 0 other;
 Alignment Scores:
 Pred..No.: 4.68e-82 Length: 8345
 Score: 750.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-884-987-2_COPY_175_319 (1-145) x AA234939 (1-8345)
 QY 1 GlyTrpLeuCysLeuLeuLeuLeuProLeuIleValTrpValLysArgLysGlu 20
 DB 4401 GGGTGGCTTGTCTCTCTTTTGGCCACTAATCCACTAATGTTGGTGAAGAGAA 4342

21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
 DB 4341 GTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCATGAATCTCAACC 4282
 QY 41 LeuAsnProGlnThrValAlaIleAsnLeuSerAspValAspLeuSerLysTrpIleThr 60
 DB 4281 TTAATCTCTGAACACACTGGCAATAAATTTATCTGATGTTGACTTGAATAATATATACACC 4222
 QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
 DB 4221 ACTATTGCTGGAGTCATGACACTAACTCAAGTTAAAGGGTTTGTTCGAAAGATGCTGTC 4162
 QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
 DB 4161 AATGAAGCCAAATAGATGATCAAGATGACAATGTCCAGACACACAGCAGAACAGAA 4102
 QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120
 DB 4101 GTTCAACTGCTTGGTAATTGGCATCAACTTCATGGAAAGAAAGCGGTATGACACATTG 4042
 QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
 DB 4041 ATTAAGATCTCAAAAAGCCAACTCTTTGACTCTTTCAGAGAAAATTCAGACTATCATC 3982
 QY 141 LeuLysAspIleThr 145
 DB 3981 CTCAGGACATTAAT 3967
 RESULT 15
 AA230948/c
 ID AA230948 standard; DNA; 8345 BP.
 AC AA230948;
 XX 23-JUL-2001 (first entry)
 DT
 XX Ahhhh survival construct.
 DE Interleukin-4 inducible epsilon promoter; human; Ige; antibody;
 KW immunoglobulin E; allergy; therapy; switch rearrangement; vector;
 KW Fas; survival construct; death gene; ds.
 XX Chimeric - Unidentified.
 XX WO200134806-A2.
 PN 17-MAY-2001.
 PD 13-NOV-2000; 2000WO-US31232.
 PF 12-NOV-1999; 99US-0165189.
 PR (RIGE-) RIGEL PHARM INC.
 PA Kinsella TM;
 PI WPI; 2001-335931/35.
 DR Screening for agents capable of inhibiting a promoter, especially
 PT interleukin-4 inducible epsilon promoter involved in immunoglobulin E
 PT production, by using diphtheria toxin constructs -
 XX Disclosure; Fig 13A-C; 80pp; English.
 XX The present sequence is that of survival construct Ahhhh in which
 CC the interleukin-4 inducible epsilon promoter-chimeric Fas(CD8 or
 CC mlyt2)-internal ribosome entry site-hydromycin-bovine growth hormone
 CC polyA tail is placed in the Cl2s vector backwards so that no leaky
 CC transcription occurs through the CMV promoter. Methods of the
 CC invention utilise diphtheria toxin for screening purposes,
 CC especially for identifying modulators of Ige synthesis, secretion
 CC and switch rearrangement. A claimed method of screening for

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	750	100.0	920	5	PCT-US95-17083-7	Sequence 7, Appli
2	750	100.0	1167	5	PCT-US95-17083-1	Sequence 1, Appli
3	750	100.0	2534	2	US-08-219-237B-1	Sequence 1, Appli
4	750	100.0	2534	4	US-08-468-560C-1	Sequence 1, Appli
5	750	100.0	2534	4	US-09-180-100-16	Sequence 16, Appli
6	750	100.0	2551	4	US-09-290-640-1	Sequence 1, Appli
7	663	88.4	857	5	PCT-US95-17083-9	Sequence 9, Appli
8	663	88.4	1104	5	PCT-US95-17083-3	Sequence 3, Appli
9	663	88.4	2471	1	US-08-444-231-18	Sequence 18, Appli
10	663	88.4	2471	1	US-08-153-443A-18	Sequence 18, Appli
11	554.5	73.9	975	5	PCT-US95-17083-5	Sequence 5, Appli
12	314.5	41.9	1480	4	US-09-290-640-65	Sequence 65, Appli

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OY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 361 GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 420
OY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
DB 421 TTAATCTCCGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATCACC 480
OY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 481 ACTATGCTGGAGTCATGACATAGCTCAAGTTAAAGGCTTTGTCGAAGAAGTGTGTC 540
OY 81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 541 AATGAAGCCAAATAGATGAGATCAAGATGACATGTCCTCAAGACACACAGACAGAAA 600
OY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaIleThrLeu 120
DB 601 GTTCAACTGCTTGGTAATTGGCATCAACTTTCATGGAAGAAAGAACGCGTATGACACATTG 660
OY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 661 ATTAAGATCTCAAAAAGCCCAATCTTGTACTCTTGACAGAAAATTCAGACTATCATC 720
OY 141 LeuLysAspIleThr 145
DB 721 CTCAGGACATTACT 735

RESULT 2
PCT-US95-17083-1
; Sequence 1, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN P4S ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; FILING DATE: PCT/US95/17083
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-1

Alignment Scores:
Pred. No.: 1,94e-88 Length: 1167
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-1 (1-1167)

OY 1 GlyTrpLeuCysLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
DB 548 GGGTGGCTTGTCTTCTTTTGGCAATTCACATTAATGTTGGTGAAGAGAAGGAA 607
OY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 608 GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 667
OY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
DB 668 TTAATCTCCGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATCACC 727
OY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
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DB 728 ACTATTGCTGGAGTCATGACACTAACTCAAGTTAAAGGCTTTGTCGAAGAAGTGTGTC 787
OY 81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 788 AATGAAGCCAAATAGATGAGATCAAGATGACATCAATGTCGAAGACACAGACAGAAA 847
OY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaIleThrLeu 120
DB 848 GTTCAACTGCTTGGTAATTGGCATCAACTTTCATGGAAGAAAGAACGCGTATGACACATTG 907
OY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 908 ATTAAGATCTCAAAAAGCCCAATCTTGTACTCTTGACAGAAAATTCAGACTATCATC 967
OY 141 LeuLysAspIleThr 145
DB 968 CTCAGGACATTACT 982

RESULT 3
US-08-219-237B-1
; Sequence 1, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY: pCEV4
; CLONE: clone pF58
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 195..1202
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: sig-peptide
; LOCATION: 195..242
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; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 243..1199
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 1831..1836
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2352..2357
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2518..2523
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
US-08-219-237B-1

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Alignment Scores:	6.09e-88	Length:	2534
Pred. No.:	Score:	Matches:	145
	750.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	2		

US-09-884-987-2_COPY_175_319 (1-145) x US-08-219-237B-1 (1-2534)

QY	1	GlyTrpLeu	CysLeuLeuLeuLeuLeuLeuProIleProLeuIleValnPrValLysArgLysGlu	20
DB	717	GGGTGGCTTGTCTCTCTTTGGCCAAATCCCACTAATGTGTGGGTGAAGAGAAAGGAA	776	
QY	21	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	40	
DB	777	GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGTTCTCATGAATCTCCAACC	836	
QY	41	LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr	60	
DB	837	TTAAATCCCTGAAACAGTGGCAATAAATTTATCTGATGTTGCATCTGAGTAAATATATCAACC	896	
QY	61	ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal	80	
DB	897	ACTATTTCGTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTGTGAAAGAATGGTGTC	956	
QY	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys	100	
DB	957	AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCACAGCACAGACAGAACAGAAA	1016	
QY	101	ValGlnLeuLeuArgAsnTrpPHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu	120	
DB	1017	GTTCACACTGCTTCGTAAATTGGCATCACTTCATCTGGAAAGAAAGAGCGTATGACACATTG	1076	
QY	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140	
DB	1077	ATTTAAGATCTCAAAAGCCATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC	1136	
QY	141	LeuLysAspIleThr	145	
DB	1137	CTCAAGGACATTACT	1151	

RESULT 4

	US-08-468-560C-1	
	; Sequence 1, Application US/08468560C	
	; Patent No. '6270998	
	; GENERAL INFORMATION:	
	APPLICANT: NATAGA, Shigekazu	
	APPLICANT: ITOH, Naoto	

QY	1	GCGTGGCTTTGCTCTCTCTTTGCCAAATCCACTAATTGTTCGGTGGAAGAGAAAAGGAA	776
Db	717	GGGTGGCTTTGCTCTCTCTTTGCCAAATCCACTAATTGTTCGGTGGAAGAGAAAAGGAA	776
QY	21	valGlnLysThrCysArgLysHisArgLysGluAsnGlnClySerHisGluSerProThr	40
Db	777	GTACAGAAAAACATGCAGAAAGCACAGAAAGAAAACAAGGTTCTCATTAATCTCCAACC	836

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QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
Db 837 TTAATCTGCTGAACAGCTGCCAATAATTTATCTGATGCTGACTTGATTAATATATACACC 896
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCGAAGAAGATGGTGC 956
QY 81 AsnGluAlaLysIleAspGluLeuLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
Db 957 AATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAAGACACAGACAGAA 1016
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
Db 1017 GTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAGACGGTATGACACATG 1076
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
Db 1077 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136
QY 141 LeuLysAspIleThr 145
Db 1137 CTCAGGACATTACT 1151
RESULT 5
US-09-180-100-16
; Sequence 16, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, NO. 630639510
; APPLICANT: NAKAMURA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-180-100-16
Alignment Scores:
Pred. No.: 6,09e-88 Length: 2534
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4
US-09-884-987-2_COPY_175_319 (1-145) x US-09-180-100-16 (1-2534)
QY 1 GlyTyrLeuCysLeuLeuLeuLeuProLeuLeuValTyrValLysArgLysGlu 20
Db 717 GGGTGGCTTTGCTCTCTTTTGCCTAATTCACCTAATTTGTTGGTGAAGAAGAA 776
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 777 GTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCATGAATCTCCAACC 836
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
Db 837 TTAATCTGCTGAACAGCTGCCAATAATTTATCTGATGCTGACTTGATTAATATATACACC 896
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCGAAGAAGATGGTGC 956
QY 81 AsnGluAlaLysIleAspGluLeuLysAsnAspValGlnAspThrAlaGluGlnLys 100
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```
Db 957 AATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCAAAGACACAGACAGAA 1016
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
Db 1017 GTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAGACGGTATGACACATG 1076
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
Db 1077 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136
QY 141 LeuLysAspIleThr 145
Db 1137 CTCAGGACATTACT 1151
RESULT 6
US-09-290-640-1
; Sequence 1, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221)..(1228)
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 267
; ISSUE: 15
; PAGES: 10709-10715
; DATE: 1992-05-25
; DATABASE ACCESSION NUMBER: X63717/Genbank
; DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1
Alignment Scores:
Pred. No.: 6,15e-88 Length: 2551
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4
US-09-884-987-2_COPY_175_319 (1-145) x US-09-290-640-1 (1-2551)
QY 1 GlyTyrLeuCysLeuLeuLeuLeuProLeuLeuValTyrValLysArgLysGlu 20
Db 743 GGGTGGCTTTGCTCTCTTTTGCCTAATTCACCTAATTTGTTGGTGAAGAAGAA 802
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 803 GTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCATGAATCTCCAACC 862
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
Db 863 TTAATCTGCTGAACAGCTGCCAATAATTTATCTGATGCTGACTTGATTAATATATACACC 922
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 923 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCGAAGAAGATGGTGC 982
QY 81 AsnGluAlaLysIleAspGluLeuLysAsnAspValGlnAspThrAlaGluGlnLys 100
```

Db 983 AATGAAGCCAAATAGATGAGATCAAGATGACAATCTCCAAAGACAGACAGACAGAAA 1042
Qy 101 ValGlnLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120
Db 1043 GTTCAACTGCTTCGTAATGTCATCAACTCACTGAAAGAAAGAGGATGATGACACATTG 1102
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleLeu 140
Db 1103 ATTAAGATCTCAAAAAGCAATCTTTGTACTCTTCAGAGAAAATTCAGACTATATC 1162
Qy 141 LeuLysAspIleThr 145
Db 1163 CTCAAGGACATTACT 1177

RESULT 7

PCT-US95-17083-9

; Sequence 9, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: CONCURRENTLY HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 857 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US95-17083-9

Alignment Scores:

Pred. No.:	2,77e-77	Length:	857
Score:	663.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.40%	Indels:	0
DB:	5	Gaps:	0

US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-9 (1-857)

Qy 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
Db 283 GTGAAGAGAAGGAAGTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGTTCT 342
Qy 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
Db 343 CATGAATCTCCACCTTAATCTGGAAGAGTGAACAGTGGCAATAATTTATCTGATGTTGACTG 402
Qy 56 SerLysThrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
Db 403 AGTAAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 462
Qy 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95
Db 463 CGAAGAATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 522
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGlu 115
Db 523 ACAGCAGAACAGAAAGTCAACTGCTCGTAATTGGCATCACTCACTCACTCACTCACTCACTCACT 582
Qy 116 AlaTyrAspThrLeuLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135
Db 583 CGGTATGACATGATTAAGATCTCAAAAAGCCATCTTTGTACTCTTGTACTCTTGTACTCTTGTACT 642
Qy 136 IleGlnThrIleLeuLysAspIleThr 145
Db 643 ATTCAGACTATCATCTCTCAAGGACATTACT 672

RESULT 8

PCT-US95-17083-3

; Sequence 3, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: CONCURRENTLY HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1104 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US95-17083-3

Alignment Scores:

Pred. No.:	4,02e-77	Length:	1104
Score:	663.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.40%	Indels:	0
DB:	5	Gaps:	0

US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-3 (1-1104)

Qy 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
Db 530 GTGAAGAGAAGGAAGTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGTTCT 589
Qy 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
Db 590 CATGAATCTCCACCTTAATCTGGAAGAGTGAACAGTGGCAATAATTTATCTGATGTTGACTG 649
Qy 56 SerLysThrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
Db 650 AGTAAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 709
Qy 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95
Db 710 CGAAGAATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 769
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGlu 115
Db 770 ACAGCAGAACAGAAAGTCAACTGCTCGTAATTGGCATCACTCACTCACTCACTCACTCACTCACT 829
Qy 116 AlaTyrAspThrLeuLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135
Db 830 CGGTATGACATGATTAAGATCTCAAAAAGCCATCTTTGTACTCTTGTACTCTTGTACTCTTGTACT 889
Qy 136 IleGlnThrIleLeuLysAspIleThr 145
Db 890 ATTCAGACTATCATCTCTCAAGGACATTACT 919

RESULT 9

US-08-444-231-18

; Sequence 18, Application US/08444231

; Patent No. 5652210

; GENERAL INFORMATION:

; APPLICANT: BARR, PHILIP J.

; APPLICANT: SHAPIRO, JOHN P.

; APPLICANT: KIEFER, MICHAEL C.

; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/444,231
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-444-231-18

Alignment Scores:
Pred. No.: 1,32e-76 Length: 2471
Score: 663.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.40% Indels: 0
DB: 1 Gaps: 0

US-09-884-987-2_copy_175_319 (1-145) x US-08-444-231-18 (1-2471)

QY	16	VallYsArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer	35
DB	699	GTGAAGAGAAAGAGAGTACAGAAACATCGAAGAACACAGAAAGAAACCAAGGTCT	758
QY	36	HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu	55
DB	759	CATGAATCTCAACCTTAAATCTGAAACAGTGCATTAATTTATCTGATGTGACTTG	818
QY	56	SerLysTyrlleThrThrleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal	75
DB	819	AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTT	878
QY	76	ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp	95
DB	879	CGAAGAAAGGTGCTCAATGAAGCAAAATAGATGAGATCAAGATGACATGCCAAGAC	938
QY	96	ThrAlaGlnGlnLysValGlnLeuLeuArgAsnTriPHisGlnLeuHisGlyLysGlu	115
DB	939	ACAGCAGACAGAAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	998
QY	116	AlaTyAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys	135
DB	999	GGGTATGACACATTTGATTAAAGATCTCAAAAAAGCCCAATCTTTGTACTCTTGCAGAGAA	1058

QY 136 IleGlnThrIleIleLeuLysAspIleThr 145
DB 1059 ATTCAGACTATCATCTCTCAAGGACATTACT 1088
RESULT 10
US-08-152-443A-18
Sequence 18, Application US/08152443A
Patent No. 5663070
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-152-443A-18

Alignment Scores:
Pred. No.: 1,32e-76 Length: 2471
Score: 663.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.40% Indels: 0
DB: 1 Gaps: 0

US-09-884-987-2_copy_175_319 (1-145) x US-08-152-443A-18 (1-2471)

QY	16	VallYsArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer	35
DB	699	GTGAAGAGAAAGAGTACAGAAACATCGAAGAACACAGAAAGAAACCAAGGTCT	758
QY	36	HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu	55
DB	759	CATGAATCTCAACCTTAAATCTGAAACAGTGCATTAATTTATCTGATGTGACTTG	818
QY	56	SerLysTyrlleThrThrleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal	75

Db 819 AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 878
Qy 76 ArglyAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95
Db 879 CGAAGAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATGTCACAGAC 938
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGlu 115
Db 939 ACAGCAGACAGAAAGTCACTGCTCGTAATGGCATCAACTTCATGGAAGAAAGAA 998
Qy 116 AlaTrpAspThrLeuIleLysAspLeuLysAlaAsnLeuCysThrLeuAlaGluLys 135
Db 999 GCGTATGACACATGATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAAA 1058
Qy 136 IleGlnThrIleLeuLysAspIleThr 145
Db 1059 ATTCAAGACTATCATCTCAAGGACATTAAT 1088
RESULT 11
PCT-US95-17083-5
; Sequence 5, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT: SECRETED HUMAN FAS ANTIGEN
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-5
Alignment Scores:
Pred. No.: 4.8e-63 Length: 975
Score: 554.50 Matches: 117
Percent Similarity: 80.69% Conservative: 0
Best Local Similarity: 80.69% Mismatches: 1
Query Match: 73.93% Indels: 28
DB: 5 Gaps: 1
US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-5 (1-975)
Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
Db 439 GGGTGGCTTTGCTCTCTCTTTTGGCAATTCACATAATTTGTTGGG----- 484
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 484 ----- 484
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
Db 485 -----GAAACAGTGGCAATAAATTTATCTGATGTTGACITGAGTAAATATATACCC 535
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 536 ACTATTGCTGGATCATGACACTAAGTCAAGTAAAGGCTTTGTTCCGAAAGAAATGTTGTC 595
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 596 AATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120

Db 656 GTTCAACTGCTTCTTAATTGTCATCAACTTCATGGAAGAAAGCGTATGACACATTG 715
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Db 716 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTCAGAGAAAATTCAGACTATCATC 775
Qy 141 LeuLysAspIleThr 145
Db 776 CTCAGGACATTAAT 790
RESULT 12
US-09-290-640-65
; Sequence 65, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussan, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 65
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1033)
; PUBLICATION INFORMATION:
; JOURNAL: J. Immunol.
; VOLUME: 148
; PAGES: 1274-1297
; DATE: 1992-02-15
; DATABASE ACCESSION NUMBER: M83649/Genbank
; DATABASE ENTRY DATE: 1994-04-18
US-09-290-640-65
Alignment Scores:
Pred. No.: 1.83e-31 Length: 1480
Score: 314.50 Matches: 69
Percent Similarity: 66.67% Conservative: 27
Best Local Similarity: 47.92% Mismatches: 43
Query Match: 41.93% Indels: 5
DB: 4 Gaps: 3
US-09-884-987-2_COPY_175_319 (1-145) x US-09-290-640-65 (1-1480)
Qy 2 Trp---LeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
Db 560 TGGTTGTTGACCATCCCTTGTTTGTAAATCCACTT---GTATTTATATATCGAAAGTAC 616
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 617 CGGAAAAGAAAGTCTGCGAAAAGGACAGACGATGACCCCT-----GAATCTAGAACC 667
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
Db 668 TCCAGTGGTGAACACCATACCAATCAATGCGCTCAAACTTTAGCTTGAGTAATATACATCCG 727
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 728 AGAATTCCTGAAGACATGACAAATCCAGAGCTTAAAAAATTTGCTCCGAGAAAATAACATC 787
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 788 AAGGAGCGCAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120
Db 848 GTCCAGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907

QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
||||| |||||||
Db 908 ATCAAGGCTCAAAAAGCGGAATGTCGAGAACCTTAGATAAAATTCAGGACATGGTC 967
QY 141 LeuLysAspIle 144
|||||
Db 968 CAGAAGGACCTT 979

RESULT 13

PCT-US95-17083-15
Sequence 15, Application PC/TUS9517083
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: " CONCURRENTLY HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/371,263
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-17083-15

Alignment Scores:
Pred. No.: 0.000157 Length: 257
Score: 99.50 Matches: 22
Percent Similarity: 55.00% Conservative: 0
Best Local Similarity: 55.00% Mismatches: 3
Query Match: 13.27% Indels: 15
DB: 5 Gaps: 1

US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-15 (1-257)

QY 1 GlyTrpLeuLysLeuLeuLeuProLeuIleValTrpValLysArgLysGlu 20
|||||
Db 158 GGGTGGCTTTGCTCTCTCTTCCCAATTCCTCAATTTGTTGGTGAAG----- 208
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
|||||
Db 209 -----CTTGGATCCGGAGAGCTCCCAACG 232

RESULT 14

US-09-221-017B-149/c
Sequence 149, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PPI182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PPI546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...478
US-09-221-017B-149

Alignment Scores:
Pred. No.: 0.075 Length: 478
Score: 82.00 Matches: 31
Percent Similarity: 46.83% Conservative: 28
Best Local Similarity: 24.60% Mismatches: 45
Query Match: 10.93% Indels: 22
DB: 4 Gaps: 5

US-09-884-987-2_COPY_175_319 (1-145) x US-09-221-017B-149 (1-478)

QY 27 LysHisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnProGluThr--- 45
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Db 386 AAGCATGATCGAACAATCGGACGACTCTAATTCGCGGAGAAATAACAAGAGCGCAAA 327
QY 46 -----ValAlaIleAsnLeuSerAspValAspLeuSerLysTyr 58
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Db 326 CTCTACATCGAGACCTATGGCTGCCAGATGAACGTACCGCAGTGGTG----- 276
QY 59 IleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsn 78
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QY 79 GlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGlu 98
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Db 233 AAGGTGGATGAGCGGATACGATCCTGGTCAATACCTGTCGTACGGGACAAATCGCGAG 174
QY 99 GlnLysVal---GlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyr 117
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QY 118 AspThrLeuLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGln 137
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QY 138 ThrIleLeuLysAsp 143
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RESULT 15

US-08-444-005-14
; Sequence 14, Application US/08444005
; Patent No. 5674734
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Seed, Brian
; APPLICANT: Stanger, Ben Z.
; APPLICANT: Lee, Tae-Ho
; APPLICANT: Kim, Emily
; TITLE OF INVENTION: CELL DEATH PROTEIN
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,005
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,164
; REFERENCE/DOCKET NUMBER: 00383/026001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-444-005-14

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Best Local Similarity: 29.79% Mismatches: 36
Query Match: 10.87% Indels: 13
DB: 1 Gaps: 4

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Qy	44	GlutThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThrThrIleAla	63
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Qy	64	GlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyValAsnGluAla	83
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Qy	84	LysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLysVal---	102
Db	1837	CAGATCGATGAATCATCGACCATGACTATGAAAGAGACTGAAAGAGAAAGTTTACCA	1896
Qy	103	LeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAla	116

Db 1897 ATGCTTCAGAAAGTGGCTGATCGGGAAGGACCAAAAGGGGCC 1938
Search completed: June 15, 2003, 22:59:24
Job time : 69 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 22:33:24 ; Search time 130 Seconds

(without alignments)
1615.145 Million cell updates/sec

Title: US-09-884-987-2_COPY_175_319

Perfect score: 750

Sequence: 1 GWCLLLPLPLVWKRKE.....KANCLTLAEKIQIILKDIIT 145

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0984987 -ECGN_1_1_104_erunat_09062003_140302_13292
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Database : PublishedApplications.NA.*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	750	100.0	2534	10	US-09-884-987-1
3	750	100.0	2551	10	US-09-802-669-1
4	750	100.0	8282	9	US-09-966-976A-7

Alignment Scores:
Pred. No.: 2,79e-87 Length: 2534
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

ALIGNMENTS

RESULT 1
US-09-949-713-16
; Sequence 16, Application US/09949713
; Patent No. US20020044944A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. US20020044944A110
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-713-16

Sequence 7, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 102, App
Sequence 17113, A
Sequence 2490, Ap
Sequence 3156, Ap
Sequence 938, App
Sequence 101, App
Sequence 13045, A
Sequence 15171, A
Sequence 7395, A
Sequence 65, Appl
Sequence 99, Appl
Sequence 98, Appl
Sequence 919, App
Sequence 218, Appl
Sequence 6140, Ap
Sequence 495, App
Sequence 1, Appli
Sequence 15, Appl
Sequence 13, Appl
Sequence 103, App
Sequence 138, App
Sequence 138, App
Sequence 647, App
Sequence 6, Appli
Sequence 14730, A
Sequence 4, Appli
Sequence 1804, Ap
Sequence 188, App
Sequence 20550, A
Sequence 3784, Ap
Sequence 8513, Ap
Sequence 7040, Ap
Sequence 3000, Ap
Sequence 1, Appli
Sequence 1464, Ap
Sequence 29, Appl
Sequence 2, Appli

Query Match:	100.00%	Indels:	0
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QY	21	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	40
DB	4341	GTACAGAAACATGCAGAAAGCAGAGAAAGCAACCAAGGTTCTCATGAATCTCCAACC	4282
QY	41	LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr	60
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QY	61	ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal	80
DB	4221	ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTGCAAGAAATGGTGTC	4162
QY	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys	100
DB	4161	AATCAAGCCAAATAGATGAGATCAAGAATGCACATGCTCCAGACACAGCAGAACAGAAA	4102
QY	101	ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu	120
DB	4101	GTTCAACTGCTGCTAATTGGCATCAACTTCATGTTGAAAGAAAGCGTATGACACATTG	4042
QY	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140
DB	4041	ATTAAAGATCTCAAAAGGCAATCTTTGTACTCTTTCAGAGAGAAAATTCAGACTATCATC	3982
QY	141	LeuLysAspIleThr 145	
DB	3981	CTCAAGGACATTACT 3967	
RESULT 5			
US-09-963-206B-7/c			
; Sequence 7, Application US/09963206B			
; Patent No. US20020123076A1			
; GENERAL INFORMATION:			
; APPLICANT: Ferrick, David A.			
; APPLICANT: Swift, Susan E.			
; APPLICANT: Fox, Bryan			
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and			
; FILE OF INVENTION: Secretion and Switch Rearrangement			
; FILE REFERENCE: A-66038-3/RMS/JJD/DLR			
; CURRENT APPLICATION NUMBER: US/09/963, 206B			
; CURRENT FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US 09/076, 624			
; PRIOR FILING DATE: 1998-05-12			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 7			
; LENGTH: 8282			
; TYPE: DNA			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: synthetic			
US-09-963-206B-7			
Alignment Scores:			
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
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Db 4401 GGGTGGCTTGTCTCTCTTTGGCAATTCACATAATGTTGGTGAAGAGAA 4342
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 4341 GTACAGAAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 4282
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThr 60
Db 4281 TTAATCTCGAACAGCTGCGCAATAATTTATCTGATGTTGACTTGCAGTAAATATATCACC 4222
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 4221 ACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGGAAGAAATGGTGTG 4162
Qy 81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 4161 AATGAAGCCAAATAGATGAGATCAAGATGACATGTCGAAGACACAGACAGAA 4102
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120
Db 4101 GTTCAACTGCTTCGTAATGGCATCACTTCAAGTGAAGAAAGAAAGCGTATGACACATTG 4042
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
Db 4041 ATTAAGATCTCAAAAAGCCAACTTTGTACTCTTGCAGAGAAAATTCAGACTATCATC 3982
Qy 141 LeuLysAspIleThr 145
Db 3981 CTCAGGACATTACT 3967
RESULT 6
US-09-966-976A-8/C
; Sequence 8, Application US/09966976A
; Patent No. US20020168649A1
; GENERAL INFORMATION:
; APPLICANT: Ferrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Syn
; TITLE OF INVENTION: Secretion and Switch Rearrangement
; FILE REFERENCE: A-66038-4/RMS/JJD/DLR
; CURRENT APPLICATION NUMBER: US/09/966, 976A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 09/076, 624
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8345
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-966-976A-8
Alignment Scores: Length: 8345
Pred. No.: 1,62e-86 Matches: 145
Score: 750.00
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Query Match: 100.00% Indels: 0
Gaps: 9
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Qy 1 GlyTrpLeuCysLeuLeuLeuProLeuValTrpValValArgLysGlu 20
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Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40

Db 4341 GTACAGAAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 4282
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThr 60
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Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 4221 ACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGGAAGAAATGGTGTG 4162
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Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120
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Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
Db 4041 ATTAAGATCTCAAAAAGCCAACTTTGTACTCTTGCAGAGAAAATTCAGACTATCATC 3982
Qy 141 LeuLysAspIleThr 145
Db 3981 CTCAGGACATTACT 3967
RESULT 7
US-09-963-206B-8/C
; Sequence 8, Application US/09963206B
; Patent No. US20020123076A1
; GENERAL INFORMATION:
; APPLICANT: Ferrick, David A.
; APPLICANT: Swift, Susan E.
; APPLICANT: Armstrong, Randall
; APPLICANT: Fox, Bryan
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige
; TITLE OF INVENTION: Secretion and Switch Rearrangement
; FILE REFERENCE: A-66038-3/RMS/JJD/DLR
; CURRENT APPLICATION NUMBER: US/09/963, 206B
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/076, 624
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8345
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-963-206B-8
Alignment Scores: Length: 8345
Pred. No.: 1,62e-86 Matches: 145
Score: 750.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 10
DB:
US-09-884-987-2_COPY_175_319 (1-145) x US-09-963-206B-8 (1-8345)
Qy 1 GlyTrpLeuCysLeuLeuLeuProLeuValTrpValValArgLysGlu 20
Db 4401 GGGTGGCTTGTCTCTCTTTGGCAATTCACATAATGTTGGTGAAGAGAA 4342
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 4341 GTACAGAAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 4282
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThr 60

4281	TTAATTCCTGAACACAGTGGCAATAAATTATCTGATGTGTGCACCTTGAGTAAATATATCATCC	4222
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4221	ACTATTGCTGGAGTCTATGACACTTAAGTCAAAGTTAAAAGGGCTTTCTTGCGAAAGAATGGTGTC	4162
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RESULTS

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US-09-802-669-102
; Sequence 102, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussou, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-345
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn, Ver. 2.0
; SEQ ID NO 102
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(399)
US-09-802-669-102

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Db      636 ACAGCAGACAGAAAGTTCAACTGCTTCGTAAATTGGCATCAACTTCATGGRAAGAAAGNA 695
Qy      116 AlaTyrAspThrLeuIleLysAspLeuLysLysLysLysLysLysLysLysLysLys 135
Db      696 GCGTATGACACATTGATTAAAGATCTCAAAAAGCCAACTTTTGTACTCTTGCAGAGAA 755
Qy      136 IleGlnThrIleIleLeuLysAspIleThr 145
Db      756 ATTCAGACTATCATCTCAAGGACATTACT 785

RESULT 9
US-09-918-995-17119
; Sequence 17119, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17119
; LENGTH: 490.
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(490)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17119

Alignment Scores:
Pred. No.: 2,96e-70 Length: 490
Score: 611.00 Matches: 125
Percent Similarity: 96.92% Conservative: 1
Best Local Similarity: 96.15% Mismatches: 4
Query Match: 81.47% Indels: 1
DB: 9 Gaps: 0

US-09-884-987-2 COPY 175 319 (1-145) x US-09-918-995-17119 (1-490)

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Db 177 CAACGTGCTTCGTAATGGCATCAACTTCATGGAAGAAAGACCGTATGACACATTGATT 236
QY 122 LysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleLeu 141
Db 237 AAGATCTCAAAAAGCCAACTTTTGTTACTCTTCGAGAGAAAATTTCAGACTATCATCCTC 296

QY 142 LysAspIleThr 145
Db 297 AAGGACATTACT 308

RESULT 15

US-09-918-995-15171
; Sequence 15171, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15171
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(496)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15171

Alignment Scores:

Pred. No.:	4.7e-46	Length:	496
Score:	425.00	Matches:	84
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	56.67%	Indels:	0
DB:	9	Gaps:	0

US-09-884-987-2_COPY_175_319 (1-145) x US-09-918-995-15171 (1-496)

QY 62 IleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyValAsn 81
Db 65 ATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGAAAGAATGGTGCAAT 124
QY 82 GluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLysVal 101
Db 125 GAAGCCAAATAGATGAGATCAAGATGACATGTCCAGACACAGCAGAACAGAAAGTT 184
QY 102 GlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrAspThrLeuIle 121
Db 185 CAACGTGCTTCGTAATGGCATCAACTTCATGAAAGAAAGACCGTATGACACATTGATT 244
QY 122 LysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleLeu 141
Db 245 AAGATCTCAAAAAGCCAACTTTTGTTACTCTTCGAGAGAAAATTTCAGACTATCATCCTC 304
QY 142 LysAspIleThr 145
Db 305 AAGGACATTACT 316

Search completed: June 15, 2003, 23:50:14
Job time : 139 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 21:50:09; Search time 1418 Seconds
(without alignments)
1656.097 Million cell updates/sec

Title: US-09-884-987-2_COPY_175_319
Perfect score: 750
Sequence: 1 GWLCLLLPLPIVWKRK.....KANLCTLAEXIQTIIILKDIY 145

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q/cg2_1/USPTO.spool/US09884987/runat_09062003_140300_13188/app_query.fasta_1.327
-DB-EST -OPMT-fastcap -SUFFIX-p2n.tst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT-ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09884987.ecgn_1_1525.erunat_09062003_140300_13188 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estnu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hic.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: gb_gss.*
- 18: em_gss_hum.*
- 19: em_gss_inv.*
- 20: em_gss_pln.*
- 21: em_gss_vrt.*
- 22: em_gss_fun.*
- 23: em_gss_mam.*
- 24: em_gss_mus.*
- 25: em_gss_oth.*
- 26: em_gss_pro.*
- 27: em_gss_rtd.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	750	100.0	1055	14	BQ051037 AGENCOURT
2	699	93.2	417	10	AV651157
3	663	88.4	509	10	AW994695
4	656.5	87.5	776	13	BI254532 602978522
5	644.5	85.9	809	12	BF126149 601650407
6	618	82.4	676	14	W05802 za89f05.r1
7	606.5	80.9	395	10	BE070451 QV4-BF040
8	601	80.1	398	9	AA180032 zo39g12.r
9	566	75.5	460	9	AA293570 zt25h11.r
10	495	66.0	305	9	AA860068 HGBBT125
11	492	65.6	1152	14	BM922638 AGENCOURT
12	426	56.8	696	10	AV715411
13	375	50.0	932	9	AL542093
14	337	44.9	217	9	AA852070 HGBBT116
15	314.5	41.9	1437	11	AK002590 Mus muscu
16	293	39.1	735	13	BI766250 603052708
17	280	37.3	663	10	AW141748 EST291827
18	215	28.7	461	14	H02935 yj46b08.r1
19	205	27.3	954	9	AA745982 ob18912.s
20	200	26.7	827	9	AJ392468 AJ392468
21	155	20.7	1052	13	BM455788 AGENCOURT
22	149	19.9	828	13	BI838027 603083875
23	135.5	18.1	494	12	BF718215
24	135.5	18.1	577	12	BF717834
25	99	13.2	577	12	BG512043
26	92.5	12.3	562	10	AV383635
27	91	12.1	562	13	BM540069 hb17902.g
28	89.5	11.9	683	10	AV852164
29	89	11.9	394	14	BM880215
30	88.5	11.8	543	14	BM793563
31	88.5	11.8	553	14	BQ488484
32	88.5	11.8	716	10	AV383642
33	88.5	11.8	796	10	AV383307
34	88.5	11.8	1042	17	CNS05EYH
35	88	11.7	688	14	BQ240549
36	87.5	11.7	1026	17	BH147298
37	87	11.6	584	9	AI231531
38	87	11.6	998	17	CNS07ASF
39	86	11.5	653	14	BQ285491 faa30g02.
40	85.5	11.4	495	13	BJ411502
41	84.5	11.3	701	14	BQ510872
42	84.5	11.3	851	17	AZ681486
43	84	11.2	410	9	AI950629
44	83.5	11.1	611	12	BG794187
45	83.5	11.1	699	9	AJ448187

ALIGNMENTS

RESULT 1
BQ051037
LOCUS BQ051037 1055 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_6954504 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5785846
5', mRNA sequence.
ACCESSION BQ051037
VERSION BQ051037.1 GI:19810377
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1055)
AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12873 row: j column: 23
High quality sequence stop: 589.
Location/Qualifiers
1. 1055

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:5785846"
/clone_lib="NIH_MGC_71"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
352 a 221 c 215 g 267 t

BASE COUNT
ORIGIN

Alignment Scores:
Pred. No.: 6,61e-80 Length: 1055
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x B0051037 (1-1055)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
Db 326 GGGTGGCTTGTCTCTCTCTTTGGCCAAATCCCACTAATCTTTGGGTGAAGAGAAAGAA 385
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 386 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGTAATCTCCAACT 445
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
Db 446 TTAATCTCTGACACATGCAGAAATTAATATCTGATGTTGACCTGAGTAATATATACCC 505
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 506 ACTATTGCTGGAGTCATGACATCAAGTAAAGGCTTTGTTGCAAGAAATGGTGTC 565
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 566 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCACAGACAGACAGACAGAA 625
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrAspThrLeu 120
Db 626 GTTCACTGCTGCTGTAATGGCATCACTTCATGGAAAGAAAGACGGTATGACATTC 685
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
Db 686 ATTAAGATCTCAAAAAGCCAACTTTGTACTCTTTCAGAGAAATTCAGACTATCATC 745
QY 141 LeuLysAspIleThr 145
Db 746 CTCAGGACATTACT 760

RESULT 2

AV6511157
LOCUS AV6511157 417 bp mRNA linear EST 15-JAN-2002
DEFINITION AV6511157 GLC Homo sapiens cDNA clone GLCCMD03 3', mRNA sequence.
ACCESSION AV6511157

VERSION
KEYWORDS
SOURCE

AV6511157.1 GI:9872171
EST.
human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)

AUTHORS

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.

TITLE

Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE

21625106

COMMENT

Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source

1. 417
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCCMD03"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 151 a 74 c 84 g 108 t
ORIGIN

Alignment Scores:

Pred. No.: 2,66e-74 Length: 417
Score: 699.00 Matches: 134
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.20% Indels: 0
DB: 10 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AV651157 (1-417)

QY 1 GlyTrpLeuCysLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
Db 16 GGGTGGCTTGTCTCTCTCTTTGGCCAAATCCCACTAATCTTTGGGTGAAGAGAAAGAA 75
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 76 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGTAATCTCCAACT 135
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
Db 136 TTAATCTCTGACACATGCAGAAATTAATATCTGATGTTGACCTGAGTAATATATACCC 195
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 196 ACTATTGCTGGAGTCATGACATCAAGTAAAGGCTTTGTTGCAAGAAATGGTGTC 255
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 256 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCACAGACAGACAGACAGAA 315
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrAspThrLeu 120
Db 316 GTTCACTGCTGCTGTAATGGCATCACTTCATGGAAAGAAAGACGGTATGACATTC 375
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGlu 134

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Db      376 ATTAAGATCTCAAAAGCCATCTTGTGACCTTCCAGAG 417
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AW994695          509 bp      mRNA      linear      EST 05-JUN-2000
LOCUS      R01-BN0039-060200-011-a05 BN0039 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW994695
ACCESSION  AW994695
VERSION     AW994695.1 GI:8254929
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 509)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20203663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC1-BN0039-060
200-011-a05et3-2000-02-06et4-1)
Seq primer: puc 18 forward
High quality sequence stop: 509.
FEATURES             source
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                    /db_xref="taxon:9606"
                    /clone_lib="BN0039"
                    /dev_stage="Adult"
                    /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 - Ludwig Institute for Cancer Research)
                    profiles into the puc 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
BASE COUNT      205 a      83 c      99 g      122 t
ORIGIN
Alignment Scores:
Pred. No.:      7.64e-70      Length:      509
Score:          663.00      Matches:      130
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    88.40%      Indels: 0
DB:             10      Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AW994695 (1-509)

QY      16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
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Db      14 GTGAAGAGAGAGGAGTACAGAAATGTCAGAAAGCCAGAAAGCAAGGTTCT 73
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QY      36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
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56 SerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
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134 AGTAAATATATACCACTATTGCTGGAGTCAATGACACTAAGTCAAGTAAAGGCTTTGTT 193
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76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp 95
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194 CGAAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACATGTCACAGAC 253
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96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115
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254 ACAGCAGACAGAAAGTTCAACTGCTTCGTAAATGGCATCAACTTCATGGAAGAAAGAA 313
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116 AlaTyrAspThrIleLysAspLeuLysAlaAsnLeuLysAlaGluLys 135
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314 GCGTATGACACATTGATTAAGATCTCAAAAGCCCAATCTTTGTACTCTTGCAGAGAAA 373
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136 IleGlnThrIleLeuLysAspIleThr 145
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374 ATTCACTATCATCTCTCCTCAGGACATTACT 403
|||||

RESULT 4
BI254532
LOCUS      602978522F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123477 5'
DEFINITION mRNA sequence.
ACCESSION  BI254532
VERSION     BI254532.1 GI:14807044
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 776)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@email.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Incyte Genomics, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1AM1301 row: 1 column: 06
            High quality sequence stop: 757.
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                    /db_xref="taxon:9606"
                    /clone_lib="NIH_MGC_12"
                    /tissue_type="cervical carcinoma cell line"
                    /lab_host="DH10B"
                    /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                    Average insert size 1.4 kb. Library prepared by Life
                    Technologies."
BASE COUNT      276 a      136 c      151 g      213 t
ORIGIN
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Pred. No.:      8.22e-69      Length:      776
Score:          656.50      Matches:      141
Percent Similarity: 96.58%      Conservative: 0
Best Local Similarity: 96.58%      Mismatches: 4
Query Match:    87.53%      Indels: 4
DB:             13      Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x BI254532 (1-776)

QY      1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuValTrpValLysArgLysGlu 20

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21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
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114 GTACAGAAACATGCGAGAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCTCAACC 173
|||||
41 -LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleTh 60
|||||
174 TTTAAATCTGAAACAGTGGCAATAATTAATCTGATGTTGACTTGTAGTAATAATATCAC 233
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60 rThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVa 80
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234 CACTATTGTGGAGTCATGACACTAAGTCAAGTTAAAGGCTT-GTTCGAAGAATGGTGT 292
|||||
80 lAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLy 100
|||||
293 CAATGAAGCAAAATAGATGAGATCAAGATGCAATGTCACAGACAGACAGACAGAA 352
|||||
100 sValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLe 120
|||||
353 AGTTCACCTGCTCGTAATGGCATCACTTCATGGAAGAAGAGCGGTATGACACAT 412
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120 uLysLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
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413 GATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGACAGAGAAAATTCAGACTATCAT 472
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140 eLeuLysAspIleThr 145
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473 CCTCAAGGACATTACT 488

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RESULT 5
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LOCUS 601650407F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:3934273 5'
DEFINITION mRNA sequence.

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ACCESSION BF126149
VERSION BF126149.1 GI:10965189
KEYWORDS EST.
SOURCE human.

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ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 809)

NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCW74 row: n column: 02

High quality sequence stop: 635.

Location/Qualifiers

FEATURES

source

1. 809

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3934273"

/clone_lib="NIH_MGC_76"

/lab_host="PHI08 (T1 phage-resistant)"

/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site: 1:

Sf11 (ggcgcctcgcc); Site 2: Sf11 (ggcattatggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCCATTTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCCGAGCGCCGACATG-dr(30)BN-3' (where B = A,

C, G or T). Average insert size 1.85

kb (range 1.0-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT 293 a 127 c 179 g 210 t

ORIGIN

Alignment Scores:

Pred. No.: 2,446-67 Length: 809
Score: 644.50 Matches: 140
Percent Similarity: 97.24% Conservative: 1
Best Local Similarity: 96.55% Mismatches: 4
Query Match: 85.93% Indels: 4
DB: 12 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x BF126149 (1-809)

```

QY 1 GlyTrpLeuCysLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
|||||
Db 42 GGTGGCT-TGCTTCTCTTTTCCCAATTCCTACTAATGT--TGGGTGAAGAGAA 98
|||||
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
|||||
Db 99 GTACAGAAACATGCGAGAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCTCAACC 158
|||||
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
|||||
Db 159 TTAATCTCTGAAACAGTGGCAATAAATTTATCTGATGTTGACATTGAGTAATAATATCAC 218
|||||
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
|||||
Db 219 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTT-GTTCAAGAAATGGTGC 277
|||||
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100
|||||
Db 278 AATGAAGCCAAATAGATGAGATCAAGATGACATGTCCACAGACAGACAGACAGAAA 337
|||||
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrAspThrLeu 120
|||||
Db 338 GTTCAACTGCTCGTAATGGCATCAACTTCATGGAAGAAGAAAGCGTATGACACATG- 396
|||||
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
|||||
Db 397 ATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGACAGAGAAAATTCAGACTATCATC 456
|||||
QY 141 LeuLysAspIleThr 145
|||||
Db 457 CTCAGAGGACATTACT 471

```

RESULT 6

LOCUS

DEFINITION

W05802 676 bp mRNA linear EST 23-APR-1996
za89f05.r1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone
IMAGE:299745 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN
);, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

W05802.1 GI:1278534
EST.
human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 676)

Authors: Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M., Holman

, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston

, R., Williamson, A., Wohlmann, P., and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 307.
Location/Qualifiers

FEATURES

source

```
1. 676
/organism="Homo sapiens"
/db_xref="GDB:124466"
/db_xref="taxon:9606"
/clone_lib="IMAGE:299745"
/clone_lib="Soares_fetal_lung_NBHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."
231 a 127 c 138 g 171 t 9 others
```

BASE COUNT

ORIGIN

Alignment Scores:

```
Pred. No.: 3e-64 Length: 676
Score: 618.00 Matches: 126
Percent Similarity: 96.92% Conservative: 0
Best Local Similarity: 96.92% Mismatches: 2
Query Match: 82.40% Indels: 2
DB: 14 Gaps: 0
```

US-09-884-987-2_COPY_175_319 (1-145) x W05802 (1-676)

```
QY 18 ArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGlu 37
DB 17 AGAAAGGAAGTACAGAAACATGCAGAGACAGAGAAAGGAAACCAAGGTTCTCATGAA 76
QY 38 SerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLys 57
DB 77 TCTCAACCTTAAATCCTGGAACAGTGGCAATAAATTTATCTGATGTTGAGTGAATAA 136
QY 58 TyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal-Argly 77
DB 137 TATATCACCACCTATTGTTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCGAA 196
QY 77 sAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAl 97
DB 137 GAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTTCCAGACACAGC 256
QY 97 aGluGlnLysValGlnLeuLeu-ArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaT 117
DB 257 AGAAGAGAAAGTTCAACTGCTTCCGTAATTTGGCATCAACTTCATGGAAAGAAAGAGCGT 316
QY 117 yAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleG 137
DB 317 ATGACACATTTGATTAAGATCTCAAAAAGCCAACTTTGTACTCTTGCAGAGAAATTC 376
QY 137 InThrIleLeuLysAspIleThr 145
DB 377 AGACTATCATCTCTCAAGGACATTACT 402
```

RESULT 7

BE070451/c

LOCUS

QV4-BT0407-020300-122-d09 BT0407 Homo sapiens cDNA, mRNA sequence. EST 09-JUN-2000

DEFINITION

BE070451

ACCESSION

BE070451.1

VERSION

EST.

SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 395)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags:

PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

20202663

MEDLINE

Contact: Simpson A.J.G.

COMMENT

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil.

Tel.: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV4-BT0407-020

300-122-d09&t3=2000-03-02&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 50

High quality sequence stop: 395.

Location/Qualifiers

1. 395

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="BT0407"

/dev_stage="Adult"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORBESTES PCR (U.S. Letters Patent application No. 196

716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 103 a 81 c 67 g 144 t

ORIGIN

Alignment Scores:

```
Pred. No.: 3.52e-63 Length: 395
Score: 606.50 Matches: 118
Percent Similarity: 96.03% Conservative: 3
Best Local Similarity: 93.65% Mismatches: 4
Query Match: 80.87% Indels: 1
DB: 10 Gaps: 1
```

US-09-884-987-2_COPY_175_319 (1-145) x BE070451 (1-395)

```
QY 1 GlyTrpLeuCysLeuLeuLeuLeuProfileProLeuIleValTrpValLysGlu 20
DB 384 GGGTGGCTTGTCTCTCTCTTTTGGCAATTCCTAGTTGTTGGTGAAGAGAAAGAA 325
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 324 GTACGAAACATGCAGAAAGCACAGAAAGCAAGGTTCTCATGAATCTCAACACC 265
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTrpIleThr 60
DB 264 TTAATCTCTGAACACTGGCAATAAATTTATCTGATGTTGACTGAGTAAATATATCACC 205
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 204 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGAAGAAGATGTC 145
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
```


the Not-I and Eco RI sites of a modified pT7t3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.

BASE COUNT 175 a 80 c 81 g 124 t

ORIGIN

Alignment Scores:
Pred. No.: 3,32e-58 Length: 460
Score: 566.00 Matches: 112
Percent Similarity: 99.12% Conservative: 1
Best Local Similarity: 98.25% Mismatches: 1
Query Match: 75.47% Indels: 0
DB: 9 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AA293570 (1-460)

QY 32 AsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSer 51
DB 1 AACCAAGGTTCTCATGAATCTCCAACTTAAATCTCGAAGAGTGGCAATAATTTATCT 60
QY 52 AspValAspLeuSerLysThrIleThrIleAlaGlyValMetThrLeuSerGlnVal 71
DB 61 GATGTGACTTGAGTAAATATATACCACTATTCTGAGTGCATGACACATAAGTCAAGTT 120
QY 72 LysGlyPheValArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAsp 91
DB 121 AAAGGCTTTGTCGAAGAAGTGTGCAATGAAGCCAAATATAGATGAGATCAAGATGAC 180
QY 92 AsnValGlnAspThrAlaGluGlnLysValGlnLeuArgAsnTrpHisGlnLeuHis 111
DB 181 ATGTCCAGACACACAGCAAGAAAGTTCACCTGCTTAAATGGCATCACTTCAT 240
QY 112 GlyLysLysGluAlaTyrAspThrLeuIleLysAspLeuLysAlaAsnLeuCysThr 131
DB 241 GGAAGAAATAATCGTATCATCATCATGATTAAGATCTCAAAAAGCCCAATCTTGTACT 300
QY 132 LeuAlaGluLysIleGlnThrIleLeuLysAspIleThr 145
DB 301 CTTGCAGAGAAAATTCAGACTATCATCTCAAGGACATTACT 342

RESULT 10
LOCUS AA860068 305 bp mRNA linear EST 11-MAR-1998
DEFINITION HGBT125 Human Glioblastoma Cell Homo sapiens cDNA, mRNA sequence.

ACCESSION AA860068
VERSION AA860068.1 GI:2952547
KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 305)

AUTHORS Jin, H.L., Hu, S.N., Tu, C., Yuan, J.G. and Qiang, B.O.

TITLE DDRT-PCR of Human Glioblastoma Cell Line BT-325 CDNAs

JOURNAL Unpublished (1997)

COMMENT Contact: Boqin Qiang

National Laboratory of Medical Molecular Biology, CAMS & PUMC
Institute of Basic Medical Sciences, Peking Union Medical College &
Chinese Academy of Medical Sciences

5 Dong Dan San Tiao, Beijing 100005, P.R. China

Tel: (010)65236411

Fax: 8610-5240529

Email: zh357@iname.com

Seq primer: M13 Reverse Primer.

Location/Qualifiers

FEATURES

Source

1..305
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human Glioblastoma Cell"
/cell_type="Glioblastoma Cell"
/cell_line="BT-325"
/lab_host="E.coli DH5a"
/note="Organ: Brain; Vector: PCRII, Invitrogen; Total RNA

was isolated from human glioblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell. Differentially expressed PCR products were cloned and sequenced.

BASE COUNT 122 a 52 c 64 g 67 t

Alignment Scores:
Pred. No.: 6.93e-50 Length: 305
Score: 495.00 Matches: 96
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.00% Indels: 0
DB: 9 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AA860068 (1-305)

QY 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
DB 17 GTGAAGAGAAAGAGTACAGAAACATGCAGAAAGCAGAAAGAAACCAAGTTCT 76
QY 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
DB 77 CATGATCTCCAACTTAATCTCGAAGAGTGGCAATAATTTATCTGATGTTG 136
QY 56 SerLysTyrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
DB 137 ACTAAATATATACCACTATTCTGAGTGCATGACACTAAGTCAAGTTAAAGCTTTGT 196
QY 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95
DB 197 CGAAGAAGTGGTGTCAATGAAGCCAAATAGATGATCAAGATGACATGTCCAAGAC 256
QY 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHis 111
DB 257 ACAGAGAACAGAAAGTTCACCTGCTTAATGGCATCACTTCAT 304

RESULT 11

BM922638

LOCUS BM922638

DEFINITION

5', mRNA sequence.

ACCESSION

BM922638

VERSION

BM922638.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1152)

AUTHORS

NIH-MGC

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12795

row: c

column: 21

High quality sequence start: 52

High quality sequence stop: 628.

Location/Qualifiers

1..1152

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5755724"

/clone_lib="NIH-MGC-118"

/tissue_type="leukocyte"

BASE COUNT 354 a 273 c 276 g 249 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9,66e-49 Length: 1152
 Score: 492.00 Matches: 109
 Percent Similarity: 88.37% Conservatives: 5
 Best Local Similarity: 84.50% Mismatches: 10
 Query Match: 65.60% Indels: 5
 DB: 14 Gaps: 2

US-09-884-987-2_COPY_175_319 (1-145) x BM922638 (1-1152)

QY 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
 |||||
 DB 467 GTGAAGAGAAAGAAAGTACAGAAACATGCAGAAAGCAGAGAAAGCAACCAAGGTTCT 526

QY 36 HisGluSerProThrLeuAsnProGluThrValAlaLeuAsnLeuSerAspValAspLeu 55
 |||||
 DB 527 CATGAATCTCCAACTTAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACCTG 586

QY 56 SerLysTrpIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
 |||||
 DB 587 AGTAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTT 646

QY 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95
 |||||
 DB 647 CGAAAGAGTGTGTCAATGGAGCCAAATAGATGATGATCAAGATGACAATGTCCAGAC 706

QY 96 ThrAlaGluGlnLysValGlnLeuArgAsnTrpHisGlnLeuHisGlyLys---L 114
 |||||
 DB 707 CCAGCAGAAAGAGAAGTTCACCTCTTCCAAATGGGCATCAACTTCATGGGAAAGGAA 766

QY 114 ysgLuAlaTrpAspThrLeu-IleLysAspLeuLysAla---AsnLeuCysThrLeu 132
 |||||
 DB 767 AGAAGCGTATGACACCTTGGATTAAAGATCTCCAAAGAGCCCAACCTTGGACCTCTG 826

QY 133 AlaGluLysIleGlnThrIle 139
 |||||
 DB 827 GCGAGAAATTCAGAACTA 847

RESULT 12
 AV715411
 LOCUS AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5', mRNA sequence.
 DEFINITION AV715411
 ACCESSION AV715411
 VERSION AV715411.1 GI:10796928
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 696)
 AUTHORS Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
 Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
 Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
 ,G., Cheng,Z. and Han,Z.
 TITLE Homo sapiens cDNA DCB clones
 JOURNAL Unpublished (2000)
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China

FEATURES
 source
 1..696
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DCBAUC01"
 /clone_lib="DCB"
 /cell_type="dendritic cells"
 /dev_stage="mature"
 /lab_host="BM25_8"
 /note="Vector: pTriplex2; Site_1: sfiIA; Site_2: sfiIB"

BASE COUNT 210 a 141 c 156 g 189 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4,44e-41 Length: 696
 Score: 426.00 Matches: 82
 Percent Similarity: 98.82% Conservatives: 2
 Best Local Similarity: 96.47% Mismatches: 1
 Query Match: 56.80% Indels: 0
 DB: 10 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AV715411 (1-696)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuLeuProLeuIleValTrpValLysArgLysGlu 20
 |||||
 DB 430 GGGTGGCTTGTCTCTCTCTTTTGGCAATTCACCTAATTTGTTGGTGAAGAGAAAGAA 489

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProthr 40
 |||||
 DB 490 GTACAGAAACATGCAGAAAGCAGAAAGCAAGGAAACCAAGGTTCTCATGAATCTCCACC 549

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTrpIleThr 60
 |||||
 DB 550 TTAATCTCTGAACAGTGGCAATAATTTATCTGATGTTGACTTCAGTAAATATATATCACC 609

QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
 |||||
 DB 610 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGCTTTGTTCCGAAGAAGTGGTGT 669

QY 81 AsnGluAlaLysIle 85
 |||||
 DB 670 ATTGAAGCCCAACTG 684

RESULT 13
 AL542093
 LOCUS AL542093 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE009Y106 5 prime
 DEFINITION AL542093 932 bp mRNA linear EST 16-FEB-2001
 ACCESSION AL542093
 VERSION AL542093.1 GI:12873796
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 932)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequenage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..932
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DE009Y106"
 /clone_lib="LTI_FL002_P11"

Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

/lab_host="DH10B"
 /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by Life
 Technologies. Contact : Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive, Rockville
 , Maryland 20850, USA Fax : (1) 301 610-8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 270 a 210 c 233 g 218 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 9.32e-35 Length: 932
 Score: 375.00 Matches: 75
 Percent Similarity: 98.68% Conservative: 0
 Best Local Similarity: 98.68% Mismatches: 1
 Query Match: 50.00% Indels: 1
 DB: 9 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AL542093 (1-932)

Qy 1 GlyTrpLeuCysLeuLeuLeuLeuLeuLeuLeuLeuLeuValTrpValLysArgLysGlu 20
 Db 705 GGGTGGCTTCTCTCTCTTTCGCAATCCCACTAATTTGGTGGTGAAGAAAGAA 764
 Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProthr 40
 Db 765 GTACAGAAACATCGAGAACACAGAAAGAAACCAAGGTTCTCATGATCTCCRACC 824
 Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60
 Db 825 TTAATCTGTAACAGTGGCAATAAATTTATCTGATGTGACTTGAGTAAATATATACCC 884
 Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValarg 76
 Db 885 ACTATTGCTGGATCATGACACTAAGTCAAGTTAARGC-TTTGTTGCGA 931

RESULT 14
 AA852070
 LOCUS: 217 bp mRNA linear EST 06-MAR-1998
 DEFINITION HGBBTL16 Human Gliablastoma Cell Homo sapiens cDNA, mRNA sequence.
 ACCESSION AA852070
 VERSION AA852070.1 GI:2939608
 KEYWORDS EST.

SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Jin, H.L., Hu, S.N., Tu, C., Yuan, J.G. and Qiang, B.Q.
 TITLE DRRP-PCR of Human Gliablastoma Cell Line BT-325 CDNAS
 JOURNAL Unpublished (1997)
 COMMENT Contact: Boqin Qiang
 National Laboratory of Medical Molecular Biology, CAMS & PUMC
 Institute of Basic Medical Sciences, Peking Union Medical College &
 Chinese Academy of Medical Sciences
 5 Dong Dan San Tiao, Beijing 100005, P.R. China
 Tel: (010)65296411
 Fax: 8610-5240529
 Email: zh357@iname.com

Seq primer: M13 Reverse Primer.
 FEATURES
 Location/Qualifiers
 1..217
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Human Gliablastoma Cell"
 /cell_type="Gliablastoma Cell"
 /cell_line="BT-325"
 /lab_host="E.coli DH5a"
 /note="Organ: Brain; Vector: PCRII, Invitrogen; Total RNA

was isolated from human gliablastoma cell line BT325.
 Then Differential Display RT-PCR was conducted between
 normal and all-trans Retinoic Acid induced cell.
 Differentially expressed PCR products were cloned and
 sequenced.

BASE COUNT 86 a 34 c 48 g 49 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4.94e-31 Length: 217
 Score: 337.00 Matches: 66
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 98.51% Mismatches: 0
 Query Match: 44.93% Indels: 0
 DB: 9 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AA852070 (1-217)

Qy 16 VallysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
 Db 17 GTGAAGAGAGAGAGAGTACAGAAACATGCAAGAACACAGAAAGAAACCAAGTTCT 76
 Qy 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
 Db 77 CATCAATCTCAACCTTAAATCTCTGAAACACAGTGGCAATAAATTTATCTGATGTTGACTTG 136
 Qy 56 SerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
 Db 137 AGTAAATATATACCACTATTGCTGGAGTCAATGACACTAAGTCAAGTTAAAGGCTTTGTT 196
 Qy 76 ArgLysAsnGlyValAsnGlu 82
 Db 197 CGAAGAATGCTGTCATGAA 217

RESULT 15
 AK002590
 LOCUS

DEFINITION Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610012D23; tumor necrosis factor receptor superfamily, member 6, full insert sequence.
 ACCESSION AK002590
 VERSION AK002590.1 GI:12832683
 KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone:lib-RIKEN full-length enriched mouse cDNA library
 clone:0610012D23.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Tanaka, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Okawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

· JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Genome Res. 10 (11), 1757-1771 (2000)
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Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
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Marchionni, L., Washima, J., Mazzaella, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Totoy-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.,
Land and Havashizaki, Y.

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